

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 29, 2005, 18:03:57 ; Search time 4813 Seconds
(without alignments)
11114.598 Million cell updates/sec

Title: US-10-071-645-1
Perfect score: 1104
Sequence: 1 ggcacgagcgccgctg.....aaaaaaaaaaaaaaaaaaaaa 1104

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_to.*
11: gb_str.*
12: gb_by.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Description
1	1104	100.0	AX451459 Sequence
2	803.8	72.8	AR454597 Sequence
3	790	71.6	BD276315 MOLECULES
4	790	71.6	AX049462 Sequence
5	632.6	57.3	CQ776764 Sequence
6	607.2	55.0	AX451461 Sequence
7	607.2	55.0	AL356300 Homo sapi
8	607.2	55.0	AL391357 Human DNA
9	605	54.8	BC020630 Homo sapi
10	600.6	54.4	AC025224 Homo sapi
11	441	39.9	AY204501 Homo sapi
12	427.2	38.7	AX894800 Sequence
13	427.2	38.7	BD030333 Sequence
14	405.4	36.7	BD139338 Extended
15	343.8	31.1	CQ704178 Sequence
16	295.8	26.8	CQ69651 Sequence
17	282.2	25.6	AX330168 Sequence
18	282.2	25.6	AX332831 Sequence
19	282.2	25.6	AX334667 Sequence

20	282.2	25.6	411	6	AX335116	AX335116 Sequence
21	279.4	25.3	409	10	AF271156	AF271156 Rattus no
22	273.4	24.8	1592	10	AY523601	AY523601 Mus muscu
c 23	270	24.5	417	6	AR272746	AR272746 Sequence
c 24	270	24.5	417	6	AR276327	AR276327 Sequence
c 25	270	24.5	417	6	AR406602	AR406602 Sequence
c 26	270	24.5	417	6	AR440452	AR440452 Sequence
c 27	270	24.5	417	6	AR447610	AR447610 Sequence
c 28	270	24.5	417	6	AR543263	AR543263 Sequence
c 29	270	24.5	417	6	AX062848	AX062848 Sequence
c 30	270	24.5	417	6	AX367765	AX367765 Sequence
c 31	231.6	21.0	259224	2	AC109006	AC109006 Rattus no
c 32	226.8	20.5	170878	2	AC107845	AC107845 Mus muscu
c 33	226.8	20.5	248479	10	AL807249	AL807249 Mouse DNA
c 34	225.6	20.4	892	11	G29976	G29976 human STR S
c 35	224.4	20.3	237	6	CQ727202	CQ727202 Sequence
c 36	202	18.3	616	9	HS324422	HS324422 Homo sapi
c 37	165	14.9	336	6	AR563282	AR563282 Sequence
c 38	165	14.9	336	6	AX322029	AX322029 Sequence
c 39	155.8	14.1	183	6	AX894673	AX894673 Sequence
c 40	155.8	14.1	183	6	BD030206	BD030206 Sequence
c 41	133.2	12.1	695	5	CR407503	CR407503 Gallus ga
c 42	133.2	11.2	308	6	CQ427555	CQ427555 Sequence
c 43	133.2	11.2	333	6	CQ418653	CQ418653 Sequence
c 44	120.4	10.9	347	10	AF041854	AF041854 Rattus no
c 45	118.8	10.8	550	6	AX392227	AX392227 Sequence

ALIGNMENTS

RESULT 1
AX451459
LOCUS AX451459 1104 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 1 from Patent WO0212279.
ACCESSION AX451459
VERSION AX451459.1 GI:21698460
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bihain, B., Bour, B. and Bougueleret, L.
TITLE Schizophrenia related gene and protein
JOURNAL Patent: WO 0212279-A 1 14-FEB-2002;
GENSET (FR)
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1..1104
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/db_xref="taxon:9606"
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Query Match 100.0%; Score 1104; DB 6; Length 1104;
Best Local Similarity 100.0%; Pred. No. 1.3e-180;
Matches 1104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Best Local Similarity 100.0%; Pred. No. 1.3e-180;
Matches 1104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGCACGAGCGCGCGCTGACCTGTCCGCGCGCGCGGACGCGCGCGGAGAGCGG 60
Db 1 GGCACGAGCGCGCGCTGACCTGTCCGCGCGCGCGGACGCGCGCGGAGAGCGG 60
Qy 61 CCGCGCGGAGCGG 120
Db 61 CCGCGCGGAGCGG 120

QY 121 TGAGCCCTTACGGCGACGGCGGCGACGTCGGCCAGATCTTCTCTCGCGCTCGAGACA 180
Db 121 TGAGCCCTTACGGCGACGGCGGCGACGTCGGCCAGATCTTCTCTCGCGCTCGAGACA 180
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QY 241 GGAGCAAGCGGCTTGTATTGAAGATGATAGGATTCATGACGCTGCTGAAATATACCG 300
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Db 541 AAATTTAAATATAAATCCCTATATCCCATATAGAAATATAAAGATCTCAGTGCAGTA 600
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Db 661 TTGACCACTTAATGAAGCGGACCCAGGCTTTTGGAGTGTGGCATCTTCGCTGATT 720
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Db 721 TGSCGTCTCCCATGTTTACATTTATTTTAAATCTGCAAAATGTTCTGTGCACTTGGATG 780
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Db 781 TGAATGCTGTCCAGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 840
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Db 841 GAAATGATCTCTGTAGATATTTCTGTTTATTTTATTTTATTTTATTTTATTTTATTT 900
QY 901 GTGTTTAAACAAGAGAGACCTTTTCTAAGGAATGATACATAGAAAAGATTTTATTTA 960
Db 901 GTGTTTAAACAAGAGAGACCTTTTCTAAGGAATGATACATAGAAAAGATTTTATTTA 960
QY 961 AAATGAGTTGTAAGCTTGTGTTTCTTTTCTGTCGCAAGCTATCTGCCCAAGTTAATGA 1020
Db 961 AAATGAGTTGTAAGCTTGTGTTTCTTTTCTGTCGCAAGCTATCTGCCCAAGTTAATGA 1020
QY 1021 AATGGACATTTTATCTCAGAAAACACACACACACACACACACACACACACACACAC 1080
Db 1021 AATGGACATTTTATCTCAGAAAACACACACACACACACACACACACACACACACAC 1080
QY 1081 CACGAAAAAATAAAAAA 1104
Db 1081 CACGAAAAAATAAAAAA 1104

RESULT 2
AR454597
LOCUS
DEFINITION Sequence 70 from patent US 6682888.
1876 bp DNA linear PAT 20-FEB-2004

ACCESSION AR454597
VERSION AR454597.1 GI:42688066
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1876)
AUTHORS Loring,J.F., Tingley,D.W. and Edwards,C.M.
TITLE Genes expressed in alzheimer's disease
JOURNAL Patent: US 6682888-A 70 27-JAN-2004;
FEATURES Location/Qualifiers
1..1876
source /organism="unknown"
ORIGIN /mol_type="genomic DNA"
Query Match 72.8%; Score 803.8; DB 6; Length 1876;
Best Local Similarity 87.9%; Pred. No. 9,8e-129;
Matches 991; Conservative 0; Mismatches 103; Indels 34; Gaps 11;
QY 10 CAGCGCCGCTGACCCCTGTCCGCGCGGCGGGGAGCGGGCGGAGGAGCGCGCGCGG 69
Db 279 CAGCGCCGCTGACCCCTGTCCGCGCGGCGGGGAGCGGGCGGAGGAGCGCGCGCGG 338
QY 70 AGCCCCCGGACGCGACCATGTGGGAGGTGCTGCCCTACGCGACGAGAAAGCTGAGCCCT 129
Db 339 AG-CCCCCGGACGCGACCATGTGGGAGGTGCTGCCCTACGCGACGAGAAAGCTGAGCCCT 397
QY 130 ACGGCGAGCGGCGGAGCGTGGGCCAGATCTTCTCTGCGCTGCGAGACACCAAACT 189
Db 398 ACGGCGAGCGGCGGAGCGTGGGCCAGATCTTCTCTGCGCTGCGAGACACCAAACT 457
QY 190 TCTTGGCGCGGCGGAGCAAGCGCGCGCCCAAGCTGGGCGAGTGGCGGAGTGGCGGAGC 249
Db 458 TCTTGGCGCGGCGGAGCAAGCGCGCGCCCAAGCTGGGCGAGTGGCGGAGC 517
QY 250 GGGTGTATTGAAGATGATAGGATTTGATGACGTGCTGAAAAATATGACCGACAGGCAC 309
Db 518 GGGTGTATTGAAGATGATAGGATTTGATGACGTGCTGAAAAATATGACCGACAGGCAC 577
QY 310 CT-CTGGTGTCTAAT-CCCCAAAGACAAATGAGTTAAGGGAGAGAAATAGGAACCGCGTA 367
Db 578 CTCTGTGTCTAATCTCCCCAAAGACAAATGAGTTAAGGGAGAGAAATAGGAACCGCGTA 637
QY 368 ACAGTTATTGCAAAAAGCATGAAAGAGAAAGCACTTTGAAATTTTACTAGCTTG-T 426
Db 638 ACAGTTATTGCAAAAAGCATGAAAGAGAAAGCACTTTGAAATTTTACTAGCTTGCT 697
QY 427 ACCCAGATGAAATCAACAACCTGTATCTGGTAT-ATGCCCGGAGACAGATTAGCGGAAG 485
Db 698 ACCCAGATGAAATCAACAACCTGTATCTGGTATCGAGCGGGAGACAGATGAGCGGAGA 757
QY 486 GAGGAAGAGAGAGAGAAAGGCTTGGGCCCTCTACAAATAAAATAAAAAAATAATT 545
Db 758 GGAGGAGGGGAGGAGGAGGAGGCTCTGGGCTCTCTGCAAAAAATAAAAAATA 817
QY 546 TAAATAAT-----AAAATCCCTATATCC-----CATATAAGAAATAAAGA 586
Db 818 AAATAAATAATTAATAATAATAATAATTCATATATACATATATAAATAATAAAGA 877
QY 587 GTCTCAGT----GCAGTATTGGCAAAATTAATCCATTTCTTTTAAATACGGGAATAT-- 640
Db 878 GTCTCAGTTCAGCTATTGTCAAAATTAATATCCATTTCTTTTATATATACGGTGAATAT 937
QY 641 --TGCCATTATAGATCTGGATTTTG-ACCATTAAAGCGGC-ACCCAGGTTGTTG 696
Db 938 TGCCAAATATAGATCTGGATTTTGAAACCACTTAATGAAGCGGCAACACCGGTTGTTG 997
QY 697 AGGTGTTGGCATCTTCGCTGATTGGCTGTTCCTCAATGTTTACATTTTAACTTTGCA 756
Db 998 AGGTGTTGGCATCTTCGCTGATTGGCTGTTCCTCAATGTTTACATTTTAACTTTGCA 1057
QY 757 AAATGTTCTGTGCACTTCGATGTGAAATGCTGCCAGTTTATTTTATTTTATGTTGTT 816

KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 Kaser,M.R., Lal,P., Yue,H., Tang,Y.T., Baughn,M.R. and Azimzai,Y. Genes expressed in hippocampus Patent: WO 0070036-A 1 23-NOV-2000;
TITLE	Incyte Genomics, Inc. (US)
JOURNAL	Location/Qualifiers
FEATURES	source
ORIGIN	1..1581 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" /note="Incyte ID No.: 239240"
Query Match	71.6%; Score 790; DB 6; Length 1581;
Best Local Similarity	90.5%; Pred. No. 2.3e-126;
Matches	985; Conservative 0; Mismatches 70; Indels 33; Gaps 12;
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Db	1 GCGGAGGAGCGCGGGCGGAG-CGCCGACGCACCATGTGCGAGTCTGCCCTAC 59
Qy	108 GGCGACGAGACTGAGCCCCCTACGGCGACGGCGGACGTTGGCGCAGATCTTCCTGC 167
Db	60 GGCGACGAGAAGCTGAGCCCCCTACGGCGAOGGGCGGACGTTGGGCCAGATCTTCCTGC 119
Qy	168 CGCCTGCAGGACACCAACAATTCTTCGGCGCGGGCAGAACAAAGCGCGCCCACAGCTG 227
Db	120 CGCCTGCAGGACACCAACAATTCTTCGGCGCGGGCAGAACAAAGCGCGCCCACAGCTG 179
Qy	228 GGCCAGATCGCCGGGCAAGCGGGTTGTTATTGAAGATGATAGATTGATGAGTGCCTG 287
Db	180 GGCCAGATCGCCGGGCAAGCGGGTTGTTATTGAAGATGATAGATTGATGAGTGCCTG 239
Qy	288 AAAAAATATGACCGACAAGGCACCT-CTGGTGTCTAACT-CCCCAAAAGACAATGAGTTAAG 345
Db	240 AAAAAATATGACCGACAAGGCACCTCTGGTGTCTAACTCCCCCAAAGACAATGAGTTAAG 299
Qy	346 GGAGAGAATAGGAACGGCGGTAA CAGTTATTGGCAAAAAGCATGAAAGAGAAGCACTT 405
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Qy	406 TGAATTTTATTACTAGCTTG-TACCCACGATGAATCAACAACCTGTATCTGGTAT-ATG 463
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Qy	522 CAATAAATAAATAAAAAAAAAATTTAAATAATAAATCCCTATA-----566
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Qy	622 CTTTTTTAACGGG----AATATTGGCAATTATAGATCTGGATTGTC-ACCATTAATGAA 676
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Qy	677 GCGC-ACCCCGAGTGTGTTGAGGTGTGGCATTCTTCGCTGATTTCGGCTGTTCCCAATG 735
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Qy	736 TTTACATTTAATCTTGC AAAAATGGTCTCTGTGCATTTGGATGGAATGCTGCCAG 795
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REFERENCE	AUTHORS	TITLE	JOURNAL
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89
90
91
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93
94
95
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100

1. Plumb, B.
Direct Submission
Submitted (09-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
Requests: clonerquest@sanger.ac.uk
On Nov 10, 2000 this sequence version replaced qi:9797484.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 'contigs' that number of the pieces
* is not known and their order in this sequence is
* arbitrary. Gaps between the contigs requested as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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		312 - CTGGTGTCTAACT - CCCCAAGAACAATGAGTTAAGGGAGAGAAATAGGAACGGCGGTAAAC 369
		75363 CCTGGTGTCTAACTCCCCCAAGAACAATGAGTTAAGGGAGAGAAATAGGAACGGCGGTAAAC 75422
QY		370 AGTTATTGGCAAAAAGCATTGAAAAGAGAAAGCACTTTGAAATTATTACTAGCTTG-TAC 428
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QY		429 CCACGATGAATTCACCAACTCTACTCTGGTAT - ATGCCCGGAGACAGATTAGGCGA - AGG 486
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QY		487 AGGAAGAGAGAGAGAAGAAGCTTTGGGC - CCTCTACAAATAAAATAAAAAAATAAATTT 545
Db		75543 AGGAGGAGGAGGAGGAGAGGCTCTGGGCTCTCTGCHAAAATAAAAAATAAAAAATAAA 75602
QY		546 TAAAAATAAATAATCCCTATATA -----TCCCATATAAGAAATAAAAGAGTC 589
Db		75603 TAAAAATTTAAAAATAATAAAAAATTCACATATACATATAAAAAAATAAAAAAGAGTC 75662
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QY		642 GGCAATTATAGATCTGGATTTTG - ACCACTTAATGAAGCGGC - ACCCAGGTGTTTTGAGG 699
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QY		700 TGTTGGCATCTTCGCTGATTTGGCTGTTCCCAATGTTTACATTTTAATCTTGC AAAA 759
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QY		760 ATGGTTCTGTGCAC TTGGATGGAATCGCTGTCCAGTTTATTTTTTTTATGTTGTTATC 819
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QY		820 CTTGGATGPACAAAAAATTCAGAAAATGATCTCTGTAGATATTCTGTTTTTATTTTGGTCA 879

Db 75903 CTTGATGTACAAAATTCAGAAATGATCTCTAGATATTCGTGTTTATTTGGTCA 75962
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Db 76083 CTATCTGCCCAAGTTAATGCAATCGACACATTTTATGTCAGAAAACACACACAC 76142
Qy 1060 AC 1101
Db 76143 AC 76184

RESULT 8
AL391357/c
LOCUS Human DNA sequence from clone RP11-401M16 on chromosome 1, complete
DEFINITION sequence.
ACCESSION AL391357
VERSION AL391357.20 GI:16501137
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 195076)
Kimberley, A.

Direct Submission
Submitted (25-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Oct 26, 2001 this sequence version replaced gi:16304938:
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, ENBL; Sw,
SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr
RP11-401M16 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6
This sequence is the entire insert of clone RP11-401M16 The true
left end of clone RP11-72P17 is at 108464 in this sequence. The
true right end of clone RP4-749H3 is at 12964 in this sequence.
Location/Qualifiers
1. 195076
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES
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29731. 30197
/note="CpG island"
/evidence=not_experimental
74209. 75906
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/evidence=not_experimental
75757. 75801
/note="Single clone region. Assembly confirmed by
restriction digest data."
145474. 145654
/note="Sequence from overlapping clone RP11-72P17
(AL365439). Assembly confirmed by restriction digest."
155179. 155865
/note="CpG island"
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Query Match 55.0%; Score 607.2; DB 9; Length 195076;
Best Local Similarity 89.2%; Pred. No. 1.9e-94;
Matches 787; Conservative 0; Mismatches 63; Indels 32; Gaps 11;
Qy 252 GTTGTATTGAGATGATAGGATGATGACGTGCTGTAATAATATGACGCAAGCACCT 311
Db 5527 GTTGTATTGAGATGATAGGATGATGACGTGCTGTAATAATATGACGCAAGCACCT 5468
Qy 312 -CTGCTGCTACT -CCCCAAGCAATGAGTTAAGGAGAGAGATAGGAACGGCGGTAA 369
Db 5467 CCTGGTGTCTAACTCCCCCAAGACAATGAGTTAAGGAGAGAGATAGGAACGGCGGTAA 5408
Qy 370 AGTTATTGGCAAAAGCATGAAAGAGAAAGACACTTTTCAAAATTTATTACTAGCTTG-TAC 428
Db 5407 AGTTATTGGCAAAAGCATGAAAGAGAAAGACACTTTTCAAAATTTATTACTAGCTTGCTAC 5348
Qy 429 CCAGATGAATCAACAACCTGTATCTGTGTAT-ATGCCCGGAGACAGATTAGGCGA-AGG 486
Db 5347 CCAGATGAATCAACAACCTGTATCTGTGTATCAGCGCGGAGACAGATAGGCGGAGAGG 5288
Qy 487 AGGAAG 545
Db 5287 AGGAAG 5228
Qy 546 TAAATATAATAAATCCCTATA-----TCCCATATAAGAAATAAAGAGAGTC 589
Db 5227 TAAATTTTAAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5168
Qy 590 TCAGT---GCAGTATTGGCAAAATTAATCACTTTCTTTTAAATACGGG---AATATT 641
Db 5167 TCAGTTGCAGCTATTTGTCAAAATTAATATCACTTTCTTTTAAATACGGTGAATATGCG 5108
Qy 642 GGCATTATAGATCGGATTTTG-ACCATTAAAGAGCGGC-ACCCAGAGTGTGTTTGGG 699
Db 5107 GCAATTTATAGATCGGATTTTGAACCACTTAATGAAGCGGCAACACACAGGTTGTTTGGG 5048
Qy 700 TGTGGGATCTTCGCTGATTTGGCTGTTCCTCAATGTTTACATTTATTAAATCTTCGCAAAA 759
Db 5047 TGTGGCATCTTCGCTGATTTGGCTGTTCCTCAATGTTTACATTTATTAAATCTTCGCAAAA 4988
Qy 760 ATGTTCTGTGCACCTGGATGTAAGTGTGCTGCCAGTTTATTTTATTTGTTGTTATC 819
Db 4987 ATGTTCTGTGCACCTGGATGTAAGTGTGCTGCCAGTTTATTTTATTTGTTGTTATC 4928
Qy 820 CTTGGATGTACAAAAAATTCAGAAATGATCTCTGTAGATATTTCTGTTTATTTTGGTCA 879
Db 4927 CTTGGATGTACAAAAAATTCAGAAATGATCTCTGTAGATATTTCTGTTTATTTTGGTCA 4868

Db 541 TCGAATAATGGTCTGTGCACCTGCGATGGAATGCTGCCAGTTTTATTTTTTTATGCT 600

QY 813 TGTATCTCTTGGATGTACAAAAATTCAGAAATGATCTCTGTAGATATTCGTGTTTAT 872

Db 601 TGTATCTCTTGGATGTACAAAAATTCAGAAATGATCTCTGTAGATATTCGTGTTTAT 660

QY 873 TTGGTCATCTTTAGAGTTATCAGGAATGTGTTTAAACAAGAGAACTTTCTTAAGG 932

Db 661 TTGGTCATCTTTAGAGTTATCAGGAATGTGTTTAAACAAGAGAACTTTCTTAAGG 720

QY 933 ATGATACATACAAAAGATTTTATTTTAAATGAGTTGTAAGCTTGTTCTTTCTTTG 992

Db 721 ATGATACATACAAAAGATTTTATTTTAAATGAGTTGTAAGCTTGTTCTTTCTTTG 780

QY 993 CTCGAAGCTATCGCCCAAGTTAATGCAATGACACATTTTTTTATGTCAGAAAAACACA 1052

Db 781 CTCGAAGCTATCGCCCAAGTTAATGCAATGACACATTTTTTTATGTCAGAAAAACACA 840

QY 1053 CAC 1103

Db 841 CAC 891

RESULT 10

AC025224 163801 bp DNA linear HTG 07-JUL-2000

LOCUS Homo sapiens chromosome 1 clone RP11-4L9, WORKING DRAFT SEQUENCE,

DEFINITION 31 unordered pieces.

ACCESSION AC025224

VERSION AC025224.3 GI:7596970

KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 163801)

Waterston,R.H.

The sequence of Homo sapiens clone

Unpublished

2 (bases 1 to 163801)

Waterston,R.H.

Direct Submission

Submitted (07-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 444 Forest Park Parkway, St. Louis, MO 63108, USA

On Apr 19, 2000 this sequence version replaced gi:7321912.

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc/index.shtml>

----- Project Information -----

Center project name: H_NH0004109

----- Summary Statistics -----

Sequencing vector: M13; 100%

Chemistry: Dye-terminator Big Dye; 0% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 145820 bases at least Q40

Consensus quality: 150999 bases at least Q30

Consensus quality: 153111 bases at least Q20

Insert size: 185000; agarose-gel

Insert size: 160801; sum-of-contigs

Quality coverage: 3.57 in Q20 bases; agarose-gel

Quality coverage: 4.25 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence

* as soon as it is available and the accession number will be preserved.

1 1640: contig of 1640 bp in length

1641 1740: gap of unknown length

1741 3443: contig of 1703 bp in length

3444 3543: gap of unknown length

3544 4790: contig of 1247 bp in length

4791 4890: gap of unknown length

4891 6777: contig of 1887 bp in length

6778 6777: gap of unknown length

6778 8114: contig of 1237 bp in length

8115 8214: gap of unknown length

8215 9912: contig of 1698 bp in length

9913 10012: gap of unknown length

10013 11754: contig of 1742 bp in length

11755 11854: gap of unknown length

11855 14058: contig of 2204 bp in length

14059 14158: gap of unknown length

14159 18450: contig of 4292 bp in length

18451 18550: gap of unknown length

18551 22470: contig of 3920 bp in length

22471 22570: gap of unknown length

22571 26337: contig of 3767 bp in length

26338 26437: gap of unknown length

26438 30118: contig of 3681 bp in length

30119 30218: gap of unknown length

30219 33161: contig of 2943 bp in length

33162 33261: gap of unknown length

33262 37679: contig of 4418 bp in length

37680 37779: gap of unknown length

37780 41155: contig of 3376 bp in length

41156 41255: gap of unknown length

41256 45149: contig of 3894 bp in length

45150 45249: gap of unknown length

45250 50155: contig of 4906 bp in length

50156 50255: gap of unknown length

50256 53871: contig of 3616 bp in length

53872 53971: gap of unknown length

53972 58814: contig of 4843 bp in length

58815 58914: gap of unknown length

58915 63420: contig of 4506 bp in length

63421 63520: gap of unknown length

63521 67773: contig of 4253 bp in length

67774 67873: gap of unknown length

67874 73896: contig of 6023 bp in length

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73997 79302: contig of 5306 bp in length

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85486 93969: contig of 8484 bp in length

93970 94069: gap of unknown length

94070 102628: contig of 8559 bp in length

102629 102728: gap of unknown length

102729 113357: contig of 10629 bp in length

113358 113457: gap of unknown length

113458 123217: contig of 9760 bp in length

123218 123317: gap of unknown length

123318 132911: contig of 9594 bp in length

132912 133011: gap of unknown length

133012 146300: contig of 13289 bp in length

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Location/Qualifiers

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 Matches 784; Conservative 0; Mismatches 69; Indels 32; Gaps 11;
 QY 252 GTTGTATTGAAGATGATAGGATTTGATGACGTGCTGAAATAATGACCGACAAAGGCACCT 311
 Db 86226 GTTGTATTGAAGATGATAGGATTTGATGACGTGCTGAAATAATGACCGACAAAGGCACCT 86285

QY 312 -CTGCTGTCTAACT-CCCCAAGACAATGAGTTAAGGAGAGAAATAGGAACGGCGGTAAAC 369
 Db 86286 CTTGCTGTCTAACTCCCCCAAGACAATGAGTTAAGGAGAGAAATAGGAACGGCGGTAAAC 86345
 QY 370 AGTTATTGGCAAAAAGCATGAAAAGAGAAAGCACCTTTGAAAATTTATTACTAGCTTGT-TAC 428
 Db 86346 AGTTATTGGCAAAAAGCATGAAAAGAGAAAGCACCTTTGAAAATTTATTACTAGCTTGT-TAC 86405
 QY 429 CCACGATGAATCAACCAACCTGTATCTCGTAT-ATGCCCGGAGACAGATTAGGCGA-AGG 486
 Db 86406 CCACGATGAATCAACCAACCTGTATCTCGTATCAGGCCGGGAGACAGATGAGCGAGAGG 86465
 QY 487 AGGAGAGAGAGAGAGAAAGCCTTTGGGC-CCTCTACAAATAAATAAATAAATAAATAAATAA 545
 Db 86466 AGGAGAGAGAGAGAGAGAGGCTCTGGGCTCCTCTGCAAAAATAAATAAATAAATAAATAA 86525
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 Db 86526 TAAATAATAAATAAATAAATAAATTCACATATACACATATAAAGAAATAAAGAGAGCTC 86585
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 Db 86646 GCATTATAGATCTGGATTTTGAAACCACTTAATGAGCGGCAACACCAAGGTGTTTTGAGG 86705
 QY 700 TGTGGCATTCTTCGCTGATTGGCTGTTCCCAATGTTTACATTATTTAATCTTGCAAAA 759
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 QY 1000 CTATCTGCCCAAGTTAATGCAAAATGGACACATTTTATGTGAGAAAAACACACACACAC 1059
 Db 87006 CTATCTGCCCAAGTTAATGCAAAATGGACACATTTTATGTGAGAAAAACACACACACAC 87065
 QY 1060 AC 1104
 Db 87066 AC 87110

RESULT 11

AY204901

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AY204901 860 bp mRNA linear PRI 20-MAY-2003
 Homo sapiens calcium/calmodulin-dependent protein kinase II
 inhibitor alpha (CaMKIINalpha) mRNA, complete cds.

AY204901.1 GI:30959105

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 860)

Li, N. and Cao, X.

Direct Submission

Submitted (19-DEC-2002) Institute of Immunology, Second Military

Medical University, 800 Xiangyin Road, Shanghai, Shanghai 200433, China

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Matches 503; Conservative 0; Mismatches 30; Indels 4; Gaps 4;

Qy 10 CAGCGCCGCTGACCCCTGTCGCGCGCGGCGGAGCGGCGGAGGCGCGCGGCGG 69
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Qy 70 AGCCCCCGGACCGACCATGTGGAGGTGCTGCCCTACGGCGACGAGAGTGAAGCCCT 129
Db 384 AGCCCCCGGACCGACCATGTGCGAGGTGCTGCCCTACGGCGACGAGAGTGAAGCCCT 443
Qy 130 ACGCGACGCGCGGACGCTGGCCAGATCTCTCTCGCGGCTGCGGACGACCACT 189
Db 444 ACGCGACGCGCGGACGCTGGCCAGATCTCTCTCGCGGCTGCGGACGACCACT 503
Qy 190 TCTTCGCGCGCGGAGCAAGCGCGCGCGGCGGAGCGGCGGAGCGGCGGAGCGG 249
Db 504 TCTTCGCGCGCGGAGCAAGCGCGCGCGGCGGAGCGGCGGAGCGGCGGAGCGG 563
Qy 250 GGGTGTATTGAAGATGATGAGATGATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 309
Db 564 GGGTGTATTGAAGATGATGAGATGATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 623
Qy 310 CT-CTGGTGTCTAAT-CCCCAAGACATGATGTTAAGGGAGAGATAGGACCGCGTA 367
Db 624 CTCTGGTGTCTAATCTCCCGGACCAATGATGTTAAGGGAGAGATAGGACCGCGTA 683
Qy 368 ACAGTTATTGCAAAAGCATGAAAGAGAGCACTTTGAAATTTATTACTAGCTTG-T 426
Db 684 ACAGTTATTGCAAAAGCATGAAAGAGAGCACTTTGAAATTTATTACTAGCTTGCT 743
Qy 427 ACCACGATGAATCAACACCTGTATCTGGTAT-ATGCCCGGAGACAGATTTAGCGAAG 485
Db 744 ACCACGATGAATCAACACCTGTATCTGGTATCAGGCGGAGACAGATGAGCGGAGA 803
Qy 486 GAGGAGAGAGAGAGAGAGAGGCTTGGCCCTCTACAAATTAATATATATATATATAT 542
Db 804 GGAGGAGGAGGAGGAGGAGGCTTGGCCCTCTGCAAAATATATATATATATATATAT 860

RESULT 12
AX894800
LOCUS AX894800 524 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 10663 from Patent EP1033401.
ACCESSION AX894800
VERSION AX894800.1 GI:40049684
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
Expressed sequence tags and encoded human proteins
Patent: EP 1033401-A 10663 06-SEP-2000;
Genet (FR)
FEATURES
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Location/Qualifiers
1. .524
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match 38.7%; Score 427.2; DB 6; Length 524;
Best Local Similarity 97.8%; Pred. No. 8e-64;
Matches 451; Conservative 2; Mismatches 6; Indels 2; Gaps 2;

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Db 24 ATTATAGATCTGGATTTTGACCACTTAATGAAGGCGCAACCCAGGTGTTTGGAGGTG 83
Qy 703 TGGCATTCTCGCTGATTGGCTGTCCCAATGTTTACATTTAAATCTTGCAGAAATG 762
Db 84 TGGCATTCTCGCTGATTGGCTGTCCCAATGTTTACATTTAAATCTTGCAGAAATG 143
Qy 763 GTTCTGTGCACTTGGATGTGAATGCTGTCAGTTTATTTTTTATTTGTTGTTATCCTT 822
Db 144 GTTCTGTGCACTTGGATGTGAATGCTGTCAGTTTATTTTTTATTTGTTGTTATCCTT 203
Qy 823 GGATGTACAAAAATTCAGAAAAATGATCTCTGTAGATATCTGTTTATTTTGGTCATCT 882
Db 204 GGATGTACAAAAATTCAGAAAAATGATCTCTGTAGATATCTGTTTATTTTGGTCATCT 263
Qy 883 TTAGAAGTTATCAGCAATGCTTTTAAACAAGAGAGAACTTTCTAAGGAATGATACAT 942
Db 264 TTAGAAGTTATCAGCAATGCTTTTAAACAAGAGAGAACTTTCTAAGGAATGATACAT 323
Qy 943 AGAAAAAGATTTATTTTAAATAGATTGTTAAAGCTTGTGTTTCTTTGTTGCTCAAGCTA 1002
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Qy 1003 TCTGCCCAAGTTAATGCAATGGACACATTTTTTATGTCAGAAAAACACACACACACA 1062
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Db 444 CACACACACACACACACACGAAAAAAGAAAAA 484

RESULT 13
BD030333
LOCUS BD030333 524 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD030333
VERSION BD030333.1 GI:22572075
KEYWORDS JP 2001269182-A/6579.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 524)
Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 6579 02-OCT-2001;
GENSET
OS Homo sapiens (human)
PN JP 2001269182-A/6579
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES JORDAN

PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC C12N5/10.
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC G06F15/40

CC	Key	Location/Qualifiers.
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ORIGIN

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	Matches 451;	Conservative 2;	Mismatches 6;	Indels 2;	Gaps 2;
Qy	645	ATTATAGACTGTGGAATTTTG-AACCACTTAAATGAAGCGGC-ACCOCAGGTGTTTTGAGGTGT	702		
Dd	24	ATTATAGACTGTGGATTTTGAACCACTTAATGAAGCGGCAACACAGGTGTTTTGAGGTGT	83		
Qy	703	TGGCATTTCTGCTGTATTTGGCTGTTCCTCCAAATGTTTACATATTAACTTGTGCAAAAATG	762		
Dd	84	TGGCATTTCTTCGCTGATTTGGCTGTTCCTCCAAATGTTTACATATTAACTTGTGCAAAAATG	143		
Qy	763	GTTCTGTGCACTTGGGATGTCAAATGCTGTCAGTTTTTATTTTTTATTTATGTTGTATTCCTT	822		
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Dd	204	GGATGTACAAAAAATTCAGAAAAATGATCTCTGTAGATATTCTGTTTATTTTTCGGTCATCT	263		
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Dd	384	TCTGCCCAAGTTAATGCAATGACACATTTTTTATGTCAGAAAAACACACACACACACA	443		
Qy	1063	CACACACACACACACACACGAAAAAATAAAAAAAAAAAAAA	1103		
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RESULT 14	BD139338	417 bp	DNA	linear	PAT 18-SEP-2002
LOCUS	BD139338				
DEFINITION	Extended cDNA of secretory protein.				
ACCESSION	BD139338				
VERSION	BD139338.1	GI:23234283			
KEYWORDS	JP 200208182-A/90.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE
AUTHORS
TITLE
Extended cDNA of secretory protein
Bougueleret, L., Duclert, A. and Edwards, J. B. D. M.
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 417)
Patent: JP 2002508182-A 90 19-MAR-2002;

COMMENT	GENSET	
OS Homo sapiens (human)		
PN JP 2002508182-A/90		
PD 19-MAR-2002		
PR 17-DEC-1998	JP 2000539136	
PR 17-DEC-1997	US 60/069957, 09-FEB-1998	US 60/074121 PR
PR 17-DEC-1998	US 60/081563, 10-AUG-1998	US 60/096116 PI
13-APR-1998 US	BOUGUERELT, AMYRIC DUCLERT, JEAN BAPTISTE DUMAS MILNE PI	LYDIE EDWARDS

PC	C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,	
PC	C12N15/10, C12P21/02, C12Q1/68, C12N15/00, C12N5/00, C12N15/00 CC
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ORIGIN

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ORGANISM	SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	3

REFERENCE	1
AUTHORS	Liew, C.C., Marshall, W.E. and Zhang, H.
TITLE	Compositions and methods relating to osteoarthritis
JOURNAL	Patent: WO 02070737-A 49104 12-SEP-2002; Chondroacene Inc. (CA)

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FEATURES
    source
    1..366
    Location/Qualifiers
        Chondrocyte Inc. (CA)
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

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ORIGIN

Query Match 31.1%; Score 343.8; DB 6; Length 366;
Best Local Similarity 97.8%; Pred. No. 1.9e-49;
Matches 359; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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Db |||||
Qy 1 CAATGTTTACATTATTATTAATCTTGCAAAAATGGCTCTGTGCACCTTGGATGTGAAATGCTG 60
Db |||||
Qy 791 TCCAGTTTATTTTATTTTATGTTTATGTTTATCCCTTGGATGTACAAAAAATTCAGAAAATGATC 850
Db |||||
Qy 61 TCCAGTTTATTTTATTTTATGTTTATGTTTATCCCTTGGATGTACAAAAAATTCAGAAAATGATC 120
Db |||||
Qy 851 TCTGTAGATATTCTGTTTATTTTATTTTGTCTCATCTTTAGAAAGTTATCAGGAATGTGTTTAAAA 910
Db |||||
Qy 121 TCTGTAGATATTCTGTTTATTTTATTTTGG-CATCTTTAGAAAGTTATCAGGAATGTGTTTAAAA 179
Db |||||
Qy 911 CAAGAAGAGAACTTTTCTAAGGAATGATACATAGAAAAAGATTTTATTTTAAAAATCAGTTG 970
Db |||||
Qy 180 CAAGAAGAGAACTTTTCTAAGGAATGATACATAGAAAAAGATTTTATTTTAAAAATCAGTTG 239
Db |||||
Qy 971 TAAAGCTTGTGTTTCTTGTGCTGCAAGCTATCTGCCNAGTTAATGCNAATGGACACA 1030
Db |||||
Qy 240 TAAAGCTTGTGTTTCTTGTGCTGCAAGCTATCTGCCNAGTTAATGCNAATGGACACA 299
Db |||||
Qy 1031 TTTTATGTCTAGAAAAACACACACACACACACACACACACACACACACACACACACACACAC 1090
Db |||||
Qy 300 TTTTATGTCTAGAAAAACACACACACACACACACACACACACACACACACACACACACACAC 359
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Qy 1091 AAAAAA 1097
Db |||||
Qy 360 AAAAAA 366
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 29, 2005, 17:36:37 ; Search time 633 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

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Listing first 45 summaries

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2: Geneseqn1990s.*
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11: Geneseqn2003ds.*
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13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	803.8	72.8	1876	AD161702	Ad161702 Human CDN
3	790	71.6	1581	AAC87358	Aac87358 Human dev
4	699.8	63.4	1510	AX20426	Aax20426 Human sec
5	699.8	63.4	1510	ADD90210	Add90210 Novel hum
6	699.8	63.4	1510	ADG90029	Adg90029 Human CDN
7	642	58.2	2058	ADQ24238	Adq24238 Human sof
8	634.6	57.5	1850	ACN90200	Acn90200 Breast ca
9	632.6	57.3	1321	ADJ75198	Adj75198 Marker ge
10	632.6	57.3	1321	ADN04817	Adn04817 Antipsori
11	632.6	57.3	1321	ADR25935	Adr25935 Breast ca
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13	519.8	47.1	873	ABQ60975	Abq60975 PRO1489 p
14	443.2	40.1	553	ABX97604	Abx97604 cDNA enco
15	427.2	38.7	524	AAC06588	Aac06588 Human sec
16	405.4	36.7	417	ADP18899	Adp18899 Human sec
17	403.8	35.6	417	AX97632	Aax97632 Extended
18	282.2	25.6	411	ABL62340	Ab162340 Colon ade
19	282.2	25.6	411	ABL65003	Ab165003 Lung canc
20	282.2	25.6	411	ABL67288	Ab167288 Thyroid c

21	282.2	25.6	411	6	ABL66839	Abl66839 Lung canc
22	272	24.6	620	11	ACN87560	Acn87560 Breast ca
c 23	270	24.5	417	5	AAF68540	Aaf68540 Human lun
c 24	270	24.5	417	6	ABK38451	Abk38451 cDNA enco
c 25	270	24.5	417	8	ACA10780	Aca10780 Human lun
c 26	270	24.5	417	8	ABX99731	Abx99731 Lung canc
c 27	270	24.5	417	10	ADH45994	Adh45994 Human lun
c 28	270	24.5	417	12	ADE71746	Ade71746 Human lun
c 29	270	24.5	417	13	ADJ19913	Adj19913 Human lun
c 30	262	23.7	453	6	ABV97214	Abv97214 Human pan
c 31	259.4	23.5	451	11	ADT96448	Adt96448 Colon can
c 32	235.6	20.4	332	2	AAT19130	Aat19130 Human gen
c 33	197.8	17.9	549	10	ABT40422	Abt40422 Toxicity
c 34	197.8	17.9	549	12	ADP71513	Adp71513 Renal tox
c 35	185.8	16.8	299	10	ADL24606	Adl24606 Intestina
36	165	14.9	336	4	AAD23580	Aad23580 Human lun
37	165	14.9	336	10	ADD66868	Add66868 Human lun
38	165	14.9	336	10	ADE88122	Ade88122 Human lun
c 39	162.4	14.7	869	6	ABQ43208	Abq43208 Oligonucl
40	155.8	14.1	183	3	AAC06461	Aac06461 Human sec
c 41	149.8	13.6	869	6	ABQ43206	Abq43206 Oligonucl
c 42	149.8	13.6	869	6	ABQ43207	Abq43207 Oligonucl
43	146.2	13.2	654	13	ADQ52714	Adq52714 Novel can
44	144	13.0	329	2	AAQ60934	Aaq60934 Human bra

ALIGNMENTS

RESULT 1
AAD31052
ID AAD31052 standard; cDNA; 1104 BP.

AC AAD31052;

DT 18-JUN-2002 (first entry)

DE Human PAPAP cDNA.

KW Human; PAPAP protein; schizophrenia candidate gene; g34872 gene;
schizophrenia; bipolar disorder; central nervous system disorder;
psychotic disorder; mood disorder; autism; mental retardation;
psychiatric disease; anxiety disorder; impulse-control disorder;
eating disorder; cognitive disorder; personality disorder; vaccine;
chromosome 1p35-p36; neuroleptic; antialcoholic; tranquiliser;
antidepressant; nootropic; antiaddictive; ss.

OS Homo sapiens.

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FT	345..1104
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FT	polyA_site
FT	1085..1104
FT	/*tag= d
WT	WO200212279-A2.
PD	14-FEB-2002.
XX	
PF	26-JUL-2001; 2001WO-IB001891.
XX	
PR	07-AUG-2000; 2000US-0223482P.
XX	
PA	(GEST) GENSET.
XX	
PI	Bihain B, Bour B, Bougueleret L;
XX	

PA (FANP/) FAN P.
PA (ROSE/) ROSEN C A.
XX
PI Ruben SM, Feng P, Lafleur DW, Moore PA, Shi Y, Kyaw H, Li Y;
PI Zeng Z, Carter KC, Endress GA, Wei Y, Fan P, Rosen CA;
XX
XX WPI; 2003-852813/79.
DR P-PSDB; ADD90301.
XX
XX New nucleic acid molecule, useful for preparing a medicament for
PT preventing, treating or ameliorating a medical condition e.g., cancer.
XX
XX Claim 1; SEQ ID NO 25; 213pp; English.
XX
XX The invention describes novel isolated human nucleic acids. The nucleic
CC acid is useful for preparing a medicament for preventing, treating or
CC ameliorating a medical condition e.g., cancer, and in gene therapy. This
CC sequence encodes a novel human secreted protein of the invention.
XX
XX Sequence 1510 BP; 473 A; 285 C; 299 G; 450 T; 0 U; 3 Other;
SQ

Query Match 63.4%; Score 699.8; DB 10; Length 1510;
Best Local Similarity 89.7%; Pred. No. 2.7e-135;
Matches 893; Conservative 1; Mismatches 69; Indels 33; Gaps 12;

QY 141 GCGGACGTGGCCGAGATCTTCTCGCGCTGCGGAGCAGCAAGCGGTGTATT 260
Db 2 GCGGACGTGGCCGAGATCTTCTCGCGCTGCGGAGCAGCAAGCGGTGTATT 120
QY 201 GCGGAGAACAGCGCGCCCAAGCTGGCGGAGATCGCGGAGCAAGCGGTGTATT 260
Db 62 GCGGAGAACAGCGCGCG-CCAGCTGGCGGAGATCGCGGAGCAAGCGGTGTATT 120
QY 261 GAGATGATAGGATTGATGACGTGCTGAAATATATACCGACAGCACCT-CTGGTGC 319
Db 121 GAGATGATAGGATTGATGACGTGCTGAAATATATACCGACAGCACCTCTCTGGTGC 180
QY 320 TAACT-CCCCAAGACAATGAGTTAAGGAGAGAGATAGGAACGGCGGTAACTGATTGG 378
Db 181 TAACTCCCCAAGACAATGAGTTAAGGAGAGAGATAGGAACGGCGGTAACTGATTGG 240
QY 379 CAAAAAGCATGAAAAGAGAAAGCACTTTGAAATTTATTAAGTTG-TACCCACGATGA 437
Db 241 CAAAAAGCATGAAAAGAGAAAGCACTTTGAAATTTATTAAGTTG-TACCCACGATGA 300
QY 438 AATCAACACCTGTATCTGGTAT-ATGCCGGAGACGATAGGCGA-AGGAGGAGAGA 495
Db 301 AATCAACACCTGTATCTGGTAT-ATGCCGGAGACGATAGGCGGAGAGGAGGAGG 360
QY 496 GAGAGAGAGAAAGCTTTGGGC-CCTCTACAAATAAAATAAAATAAAATAAATAAATAA 554
Db 361 AGGAGGAGAGGCTCTGGGCTCTCTGCAAAATAAAATAAAATAAATAAATAAATAA 420
QY 555 AAAATCCCTATA-----TCCCATATAAGAAATAAAGAGTCTCAGT- 594
Db 421 AAAAAATAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 480
QY 595 GCAGTATTGGCAAAATTAATCCATTTCTTTTATACGGG-----AATATTGGATTATA 650
Db 481 GCTATTGTGCAAAATTAATCCATTTCTTTTATACGGGGAATATTGGCAATATA 540
QY 651 GATCTGGATTGTTG-ACCACCTTAATGAAGCGGC-ACCCAGGTGTTTGGAGTGTGGCAT 708
Db 541 GATCTGGATTGTAACCACTTAATGAAGCGGCAACACAGGTGTTTGGAGTGTGGCAT 600
QY 709 TCTTCCTGATTGGCTGTCCCAATGTTTACATTTAATCTTGCAGAAATGTTCTG 768
Db 601 TCTTCCTGATTGGCTGTCCCAATGTTTACATTTAATCTTGCAGAAATGTTCTG 660
QY 769 TGCACCTTGGATGGAATGCTGCCAGTTTATTTTTTTTATGTTTATCTCTCGATCT 828
Db 661 TGCACCTTGGATGGAATGCTGCCAGTTTATTTTTTTTATGTTTATCTCTCGATCT 720

QY 829 ACACAAAATTCAGAAAATGATCTCTGTAGATATCTGTTTATTTTGGTCATCTTTAGAA 888
Db 721 ACACAAAATTCAGAAAATGATCTCTGTAGATATCTGTTTATTTTGGTCATCTTTAGAA 780
QY 889 GTTATCAGGAATGTGTTTAAAAACAAGAGAGAACTTTTCTAAGGAATGATACATAGAAA 948
Db 781 GTTATCAGGAATGTGTTTAAAAACAAGAGAGAACTTTTCTAAGGAATGATACATAGAAA 840
QY 949 GATTTTATTTAAATAGTTGTAAGCTTGTTTCTTTTGTGTCGCAAGCTATCTGCC 1008
Db 841 GATTTTATTTAAATAGTTGTAAGCTTGTTTCTTTTGTGTCGCAAGCTATCTGCC 900
QY 1009 CAAGTTAATGCAATGGACACATTTTATCTCAGAAAAACACACACACACACACA 1068
Db 901 CAAGTTAATGCAATGGACACATTTTATCTCAGAAAAACACACACACACACACA 960
QY 1069 CACACACACACACACGAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 1104
Db 961 CACACACACACACACACACACACGAAAAAATAAATAAATAAATAAATAAATAA 996

RESULT 6
ADG90029
ID ADG90029 standard; cDNA; 1510 BP.
XX
AC ADG90029;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human cDNA from secreted protein gene 15.
XX
KW Secreted protein; gene therapy; neural disorder; immune system disorders;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; cancer; systemic lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
KW myocardial infarction; AIDS; infection; human; ss; gene.
XX
OS Homo sapiens.
XX
PN US2003166541-A1.
XX
PD 04-SEP-2003.
XX
PF 04-JUN-2002; 2002US-00160162.
XX
PR 30-JUL-1997; 97US-0054209P.
PR 30-JUL-1997; 97US-0054211P.
PR 30-JUL-1997; 97US-0054212P.
PR 30-JUL-1997; 97US-0054213P.
PR 30-JUL-1997; 97US-0054214P.
PR 30-JUL-1997; 97US-0054215P.
PR 30-JUL-1997; 97US-0054217P.
PR 30-JUL-1997; 97US-0054218P.
PR 30-JUL-1997; 97US-0054234P.
PR 30-JUL-1997; 97US-0054236P.
PR 18-AUG-1997; 97US-0055968P.
PR 18-AUG-1997; 97US-0055969P.
PR 18-AUG-1997; 97US-0055972P.
PR 19-AUG-1997; 97US-0056534P.
PR 19-AUG-1997; 97US-0056543P.
PR 19-AUG-1997; 97US-0056561P.
PR 19-AUG-1997; 97US-0056727P.
PR 19-AUG-1997; 97US-0056729P.
PR 19-AUG-1997; 97US-0056730P.
PR 26-JUN-1998; 98WO-US015949.
PR 26-JUN-1999; 99US-00236557.
PR 05-JUN-2001; 2001US-0295558P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.

XX	Ruben SM, Feng P, Lafleur DW, Moore PA, Shi Y, Kyaw H, Li Y;	
PI	Zeng Z, Carter KC, Endress GA, Wei Y, Fan P, Rosen CA;	
XX	WPI; 2003-874923/81.	
DR	P-PSDB; ADG90120.	
XX		
XX	Nucleic acids encoding 83 secreted polypeptides, useful for preventing,	
PT	diagnosing and treating disorders related to their aberrant expression	
PT	and activity.	
XX		
XX	Claim 1; SEQ ID NO 25; 309pp; English.	
XX		
CC	The invention relates to an isolated nucleic acid molecule encoding a	
CC	secreted protein that is at least 95% identical to a polynucleotide	
CC	fragment of any of the nucleotide sequences listed in table 1A of the	
CC	specification, which is hybridisable to the nucleotide sequences, a	
CC	polynucleotide encoding a polypeptide (or a polypeptide fragment, domain	
CC	or epitope of any of the amino acid sequences) listed in table 1A of the	
CC	specification, a polynucleotide which is an (allelic) variant of the	
CC	nucleotide sequences listed in the specification, a polynucleotide which	
CC	encodes a species homologue of the above amino acid sequences, a	
CC	polynucleotide capable of hybridising under stringent conditions to any	
CC	of the above polynucleotides, where the polynucleotide does not hybridise	
CC	under stringent conditions to a nucleic acid molecule having a nucleotide	
CC	sequence of only A or T residues. Also included are a recombinant vector	
CC	comprising the above nucleic acid molecule, making a recombinant host	
CC	cell comprising the above nucleic acid molecule, an isolated polypeptide	
CC	comprising a sequence that is at least 95% identical to the polypeptide	
CC	(or its fragment, domain, epitope, secreted form, (allelic) variant or	
CC	homologue) encoded by the above nucleic acid molecule, an isolated	
CC	antibody that binds specifically to the above polypeptide, a recombinant	
CC	host cell produced by the above method and that expresses the above	
CC	polypeptide, making an isolated polypeptide, preventing, treating or	
CC	ameliorating a medical condition, diagnosing a pathological condition or	
CC	a susceptibility to a pathological condition in a subject, identifying a	
CC	binding partner to the above polypeptide, the gene corresponding to the	
CC	cDNA sequence given in the specification, and identifying an activity in	
CC	a biological assay. The nucleic acid molecule and polypeptide are useful	
CC	in diagnosing, preventing, prognosing or treating diseases or disorders	
CC	associated with aberrant expression and/or activity of the above	
CC	polypeptide, such as neural disorders, immune system disorders, muscular	
CC	disorders, reproductive disorders, gastrointestinal disorders, pulmonary	
CC	disorders, cardiovascular disorders, renal disorders, proliferative	
CC	disorders and/or cancers. In particular, these diseases are systemic	
CC	lupus erythematosus, rheumatoid arthritis, multiple sclerosis	
CC	thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,	
CC	allergies, nephritis, Parkinson's disease, Alzheimer's disease,	
CC	atherosclerosis, myocardial infarction, AIDS and infections. The methods	
CC	may be used for identifying agonists and antagonists of the	
CC	polynucleotide and polypeptide. The present sequence is a cDNA from one	
CC	of the 83 disclosed secreted protein genes.	
XX		
XX	Sequence 1510 BP; 473 A; 285 C; 299 G; 450 T; 0 U; 3 Other;	
XX		
Query Match	63.4%; Score 699.8; DB 10; Length 1510;	
Best Local Similarity	89.7%; Pred. No. 2.7e-135;	
Matches	893; Conservative 1; Mismatches 69; Indels 33; Gaps 12;	
Qy	141 GGCACGTGGGCCAGATCTTCTCTCTCGCGCTGCAGGACCAACAACACTTCTTCGGCGCC 200	
Db	2 GGCACGTGGGCCAGATCTTCTCTCTCGCGCTGCAGGACCAACAACACTTCTTCGGCGCC 61	
Qy	201 GGCAGAACACCGCGGCCCAAGCTGGCCAGATCGCCGGAGACACCGGTGTATT 260	
Db	62 GGCAGAACACCGCGGCCG-CGAAGCTGGCGWAGATCGCCGGAGACACCGGTGTATT 120	
Qy	261 GAAGATGATAGGATTGATGACGTCTGAAAAATATGACCGAACAGGCACCT-CTGGTGTC 319	
Db	121 GAAGATGATAGGATTGATGACGTCTGAAAAATATGACCGAACAGGCACCTCTGGTGTC 180	
Qy	320 TAACT-CCCCAAGACAAATGAGTTAAGGGAGAGAAATAGGAACGCGCGTAAACAGTATTGG 378	

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Query Match	63.4%;	Score 699.8;	DB 10;	Length 1510;
Best Local Similarity	89.7%;	Pred. No. 2.7e-135;		
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Db	2	GGCGACGTGGGCCAGATCTTCTCTCGCGCGCTGCAGGACCAACAATCTTCTTCGGCGCC	61	
Qy	201	GGGCAGAACAGCGGCCCGCCCAAGCTGGCCAGATCGGCCGAGACCGGTTGTATT	260	
Db	62	GGGCAGAACAGCGGCCG-CCAACTGGGCWAGATCGCCCGACCAAGCGGTTGTATT	120	
Qy	261	GAAGATGATAGGATTGATGACGTCCTGAAAAATATGACCGAACAGGCACCT-CTGGTGTC	319	
Db	121	GAAGATGATAGGATTGATGACGTCCTGAAAAATATGACCGAACAGGCACCTCTCGGTGC	180	
Qy	320	TAACT-CCCCAAGACAAATGAGTTAAGGGAGAGAAATAGGAACGGCGGTAAACAGTTATTGG	378	

XX 26-NOV-2003; 2003WO-US038193.
XX PF
XX PR
XX 26-NOV-2002; 2002US-0429739P.
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX PI Aziz N, Ginsburg WM, Zlotnik A;
XX WPI; 2004-441208/41.
XX Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
XX Example 2; SEQ ID NO 7058; 210pp; English.
XX
XX The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytotatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
XX SQ Sequence 2058 BP; 488 A; 468 C; 405 G; 695 T; 0 U; 2 Other;
Query Match 58.2%; Score 642; DB 12; Length 2058;
Best Local Similarity 87.3%; Pred. No. 2.9e-123;
Matches 838; Conservative 0; Mismatches 90; Indels 32; Gaps 11;
QY 177 GACACCAACAACTTCTTCGGCGCGGCGGAGCAAGCGCGCCGAGCTGGCCAGATC 236
DB 1873 GAGACAGAACTCGATCGCTCGCGCGCTCGCGCGGAGGACCAAGCTGGCCAGATC 1814
QY 237 GCGCGGAGCAAGCGGCTTGTATTGAAGATGATGAGATTGATGATGATGATGATGATG 296
DB 1813 GCGCGGAGCAAGCGGCTTGTATTGAAGATGATGAGATTGATGATGATGATGATGATG 1754
QY 297 ACCGACAGGCACCT-CTCGTGTCTTAAC-CCCCAAGCAATGATGATGATGATGATGATG 354
DB 1753 ACCGACAGGCACCTCTCGTGTCTTAACCCCCAAGCAATGATGATGATGATGATGATGATG 1694
QY 355 AGGAACGGCGGTAACAGTTATTGGCAAAAGCATGAAAGAGAGAGCACTTTGAAATTTA 414
DB 1693 AAGAAGCGGGTAACAGTTATTGGCAAAAGCATGAAAGAGAGAGCACTTTGAAATTTA 1634
QY 415 TTACTAGCTTG-TACCACGATGAATCAACACCTGTATCTGGTAT-ATGCCCGGAGAC 472
DB 1633 TTACTAGCTTGTTACCCAGATGAATCAACACCTGTATCTGGTATCAGCGCGGAGAC 1574
QY 473 AGATTAGGCGA-AGGAGGAG 530
DB 1573 AGATTAGGCGAGAGGAG 1514
QY 531 TAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 574
DB 1513 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1454
QY 575 AGAATAAAGATCTCAGT-----GCAGTATGGCAAAATTAATTCATTTCTTTTAAAT 630
DB 1453 AATAAATAAAGATCTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGT 1394
QY 631 ACCGGAATATT-----GGCATTATAGATCTGGAATTTTG-ACCATTAAAGAGCGGC-ACC 684
DB 1393 TAGGGTGAATATGGCAATATAGATCTGGATTTTGAACCACTTAATGAAGCGGCAACA 1334

QY 685 CCAGGTGTTTGGAGTGTGGCATTTCTTCGCTGATTTGGCTGTTCCCAATGTTTACATTA 744
DB 1333 CCAGGTGTTTGGAGTGTGGCATTTCTTCGCTGATTTGGCTGTTCCCAATGTTTACATTA 1274
QY 745 TTTAATCTTGCAGAAATGTTCTGTGCACTTGGGATGTGAAATGCTGTCCAGTTTATTTT 804
DB 1273 TTTAATCTTGCAGAAATGTTCTGTGCACTTGGGATGTGAAATGCTGTCCAGTTTATTTT 1214
QY 805 TTTTATGTTTATCTTGGATGTACAAAAATTCAGAAATGATCTCTGTAGATATTTCT 864
DB 1213 TTTTATGTTTATCTTGGATGTACAAAAATTCAGAAATGATCTCTGTAGATATTTCT 1154
QY 865 GTTTTATTTTGTCTCATCTTTAGAGTGTATCAGGAATGTTTAAACCAAGAGAGAACTT 924
DB 1153 GTTTTATTTTGTCTCATCTTTAGAGTGTATCAGGAATGTTTAAACCAAGAGAGAACTT 1094
QY 925 TTCTAAGGAATGATACATAGAAAAAGATTTTATTTTAAATGATGTTGTAAGCTTGTGTTT 984
DB 1093 TTCTAAGGAATGATACATAGAAAAAGATTTTATTTTAAATGATGTTGTAAGCTTGTGTTT 1034
QY 985 CTTTGTCTGCAAGCTATCTGCCCAAGTTAATGCAAAATGGACACATTTTATGTCTAGA 1044
DB 1033 CTTTGTCTGCAAGCTATCTGCCCAAGTTAATGCAAAATGGACACATTTTATGTCTAGA 974
QY 1045 AAAAC 1104
DB 973 AAAAC 914
RESULT 8
ACN90200
ID ACN90200 standard; DNA; 1850 BP.
XX AC ACN90200;
XX DT 02-DEC-2004 (first entry)
XX DE Breast cancer related marker, seq id 11350.
XX KW Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
XX OS Homo sapiens.
XX PN US2003099974-A1.
XX PD 29-MAY-2003.
XX PF 18-JUL-2002; 2002US-00198846.
XX PR 18-JUL-2001; 2001US-0306220P.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX WPI; 2003-787014/74.
XX Novel isolated polypeptide associated with breast cancer, useful for
PT detecting presence of polypeptide in sample, as a marker for breast
PT cancer.
XX Disclosure; SEQ ID NO 11350; 36pp; English.
XX The invention relates to an isolated polypeptide (I) associated with a
CC breast cancer which is encoded by a nucleic acid molecule comprising a
CC nucleotide sequence (S1). Further disclosed is an antibody that binds to
CC the polypeptide of the invention. The activity of the polypeptide of the
CC invention may be described as cytostatic. The antibody is useful for
CC detecting the presence of (I) in a sample. Nucleic acid molecules of the
CC invention are useful in the detection of breast tumours. (I) is useful as
CC a marker for breast cancer and in breast cancer therapy. Sequences given
CC in records ACN78851-ACN92934 represent nucleic acid markers associated

CC with breast cancer. Note: The sequence listing does not form part of the
CC specification but may be obtained in electronic format from the USPTO web
CC site at seqdata.uspto.gov/sequence.html?docID=20030099974

XX SQ Sequence 1850 BP; 595 A; 349 C; 430 G; 461 T; 0 U; 15 Other;

Query Match 57.5%; Score 634.6; DB 11; Length 1850;
Best Local Similarity 86.9%; Pred. No. 9.8e-122;
Matches 833; Conservative 0; Mismatches 94; Indels 32; Gaps 11;

QY 177 GACACCAACACTCTCTGGCGCCGGCAGACAGCGCCGCCAAGCTGGCCGAGATC 236
DB 192 GAAACTCGATCGCTGCGCGCGCTGCGCCCGAGGACGATGGAAGCTGGCCGAGATC 251
QY 237 GCGCGGAGCAACGGGTTGTTATTGAAGATGATAGGATGATGCTGTAATAATATG 296
DB 252 GCGCGGAGCAACGGGTTGTTATTGAAGATGATAGGATGATGCTGTAATAATATG 311
QY 297 ACCGACAGGCACTTCTGGTGTCTAACT-CCCCAAGACAATGATGTTAAGGAGAGAT 354
DB 312 ACCGACAGGCACTTCTGGTGTCTAACTCCCCAAGACAATGATGTTAAGGAGAGAT 371
QY 355 AGAACCGCGGTAAACAGTTATTGGCAAAAGCATGAAGAGACAGCACTTTGAAATTTA 414
DB 372 AAGAACCGCGGTAAACAGTTATTGGCAAAAGCATGAAGAGACAGCACTTTGAAATTTA 431
QY 415 TTACTAGCTTG-TACCCAGATGAATCAACACCTGTATCTGGTAT-ATGCCCGGAGAC 472
DB 432 TTACTAGCTTG-TACCCAGATGAATCAACACCTGTATCTGGTATCAGCGCGGAGAC 491
QY 473 AGATTAGCGGA-AGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 530
DB 492 AGATTAGCGGA-AGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 551
QY 531 TAAACCAACCAATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 574
DB 552 TAAACCAACCAATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 611
QY 575 AAGATAAAGAGTCTCAGT-----GCAGTATTGGCAAAATTAATTAATTAATTAAT 630
DB 612 AATATAAAGAGTCTCAGTTCAGTATTGTCAGATTAATTAATTAATTAATTAATTA 671
QY 631 ACGGGAATTT---GGCATTATAGATGAGATTTTG-ACCACTTAATGAAGCGG-ACC 684
DB 672 TACGCTGAATATTGGCAATATAGATCTGGATTTTGAACCACTTAATGAAGCGGCA 731
QY 685 CCAGTGTCTTTCAGTGTGGCAATCTTGGCTGATTTGGCTTTCCCAATGTTTACATTA 744
DB 732 CCAGTGTCTTTCAGTGTGGCAATCTTGGCTGATTTGGCTTTCCCAATGTTTACATTA 791
QY 745 TTTAATCTTGCAAAATGTTCTGTGCACTGGATGTGAATGCTGTCCAGTCTTATTTT 804
DB 792 TTTAATCTTGCAAAATGTTCTGTGCACTGGATGTGAATGCTGTCCAGTCTTATTTT 851
QY 805 TTTAATGTTGTTATCTTGGATGTGTAACAAATTTAGAAATGATCTCTGTAGATATCT 864
DB 852 TTTAATGTTGTTATCTTGGATGTGTAACAAATTTAGAAATGATCTCTGTAGATATCT 911
QY 865 GTTTTATTTTGTCTATCTTAGAAGTTATCAGGATGTTTAAACCAAGAGAGACATTT 924
DB 912 GTTTTATTTTGTCTATCTTAGAAGTTATCAGGATGTTTAAACCAAGAGAGACATTT 971
QY 925 TTCTAAGGAATGATACATAGAAAGATTTTATTTTAAATGATGTTGTAAGCTCTGTTT 984
DB 972 TTCTAAGGAATGATACATAGAAAGATTTTATTTTAAATGATGTTGTAAGCTCTGTTT 1031
QY 985 CTTTGTGCTGAAGCTATCTGCCCAAGTTAATGCAATTTGACACATTTTATGTCAGA 1044
DB 1032 CTTTGTGCTGAAGCTATCTGCCCAAGTTAATGCAATTTGACACATTTTATGTCAGA 1091
QY 1045 AAAAAAC 1103
DB 1092 AAAAAAC 1150

RESULT 9

ADJ75198/c
ID ADJ75198 standard; DNA; 1321 BP.

XX AC ADJ75198;

XX DT 20-MAY-2004 (first entry)

XX Marker gene SEQ ID NO:450.

XX bronchial asthma; chronic obstructive pulmonary disease;
XX respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
XX gene therapy; marker gene; gene; ds.

XX Homo sapiens.

XX EPI394274-A2.

XX 03-MAR-2004.

XX 04-AUG-2003; 2003EP-00254857.

XX 06-AUG-2002; 2002JP-00229312.

XX 20-MAR-2003; 2003JP-00077212.

XX (GENO-) GENOX RES INC.

XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K;

XX WPI; 2004-193155/19.

XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
XX comparing the expression level of a marker gene in a biological sample
XX from a subject with the expression level of the gene in a sample from a
XX healthy subject.

XX Claim 1; SEQ ID NO 450; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma
XX or chronic obstructive pulmonary disease. The method comprises
XX determining the expression level of a marker gene in a biological sample
XX from a subject, comparing the expression level determined with the
XX expression level of the marker gene in a biological sample from a healthy
XX subject, and judging whether the subject has bronchial asthma or chronic
XX obstructive pulmonary disease. The marker gene comprises: (a) a group of
XX genes (S1) whose expression levels increase when respiratory epithelial
XX cells are stimulated with interleukin-13; or (b) a group of genes (S2)
XX whose expression levels decrease when respiratory epithelial cells are
XX stimulated with interleukin-13. Also described: (1) a reagent (1) for
XX testing for bronchial asthma or chronic obstructive pulmonary disease;
XX (2) a kit for screening for a candidate compound for a therapeutic agent
XX to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
XX an animal model for bronchial asthma or chronic obstructive pulmonary
XX disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
XX method for producing an animal model for bronchial asthma or chronic
XX obstructive pulmonary disease; (6) a therapeutic agent for bronchial
XX asthma or chronic obstructive pulmonary disease, comprising the compound,
XX a marker gene or an antisense nucleic acid corresponding to a portion of
XX the marker gene, a ribozyme, a polynucleotide that suppresses the
XX expression of the gene through an RNAi effect or an antibody recognising
XX a protein encoded by a marker gene; and (7) a DNA chip for testing for
XX bronchial asthma or a chronic obstructive pulmonary disease, on which a
XX probe has been immobilised to assay a marker gene. (1) has respiratory
XX and antiasthmatic activities, and can be used in gene therapy. The method
XX is useful for testing for or screening for a therapeutic agent for
XX bronchial asthma or chronic obstructive pulmonary disease. The present
XX sequence is used in the exemplification of the present invention.

XX SQ Sequence 1321 BP; 414 A; 255 C; 236 G; 416 T; 0 U; 0 Other;

Query Match 57.3%; Score 632.6; DB 12; Length 1321;

Best Local Similarity 89.0%; Pred. No. 2.3e-121;
Matches 816; Conservative 0; Mismatches 69; Indels 32; Gaps 11;

```
QY 220 CCAAGCTGGCCGACATCGCGGAGCAGAGCGGGTGTATTGAAGATGATAGGATTGATG 279
Db 1321 CCAAGCTGGCCGACATCGCGGAGCAGAGCGGGTGTATTGAAGATGATAGGATTGATG 1262
QY 280 ACGTGTGAAAAATATGACGCGACAGGCACCT-CTGGTGTCTAACT-CCCCAAAGACAAT 337
Db 1261 ACGTGTGAAAAATATGACGCGACAGGCACCTCTGTGTCTAACTCTCCCAAGACAAT 1202
QY 338 GAGTTAAGGAGAGAAATAGGAACGGCGGTAAACAGTTATTGGCAAAAAGCATGAAAAGAGA 397
Db 1201 GAGTTAAGGAGAGAAATAGGAACGGCGGTAAACAGTTATTGGCAAAAAGCATGAAAAGAGA 1142
QY 398 AAGCACTTTGAAATTTATTACTAGCTTG-TACCCAGATGAATCAACACCTGTATCTG 456
Db 1141 AAGCACTTTGAAATTTATTACTAGCTTG-TACCCAGATGAATCAACACCTGTATCTG 1082
QY 457 GTAT-ATGCCCGGAGACAGATTAGGCGA-AGGAGGAGAGAGAGAGAAAGGCTTGGG 514
Db 1081 GTATCAGCGCGGAGACAGATTAGGCGA-AGGAGGAGAGAGAGAGAAAGGCTTGGG 1022
QY 515 C-CCTCTACAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 566
Db 1021 CTCCTCTGCAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 962
QY 567 -----TCCCATATAGAAATAAAGAGTCTCAGT-----GCAGTATTGGCAAAATTA 613
Db 961 TATATACATATATAAAGAAATAAAGAAAGTCTCAGTTCGACGATATTTCGCAAAATTAAT 902
QY 614 ATCCATTCTCTTTTAATACGGG----AATATTGGCATTATAGATCTGGATTTTG-ACCAC 668
Db 901 ATCCATTCTCTTTATACGGGTGATATTGGCATTATAGATCTGGATTTTG-ACCAC 842
QY 669 TTAATGAAGCGG-ACCACAGGTTTGGAGTGTGGCATCTTCGCTGATTTGGCTGT 727
Db 841 TTAATGAAGCGGCAACACAGGTTTGGAGTGTGGCATCTTCGCTGATTTGGCTGT 782
QY 728 TCCCAATGTTTACATTTTAACTCTGCAAAATGTTCTGTGCACTTGGATGTGAATG 787
Db 781 TCCCAATGTTTACATTTTAACTCTGCAAAATGTTCTGTGCACTTGGATGTGAATG 722
QY 788 CTGTCCAGTTTATTTTTTTATGTTTATCTCGATGTATCAAAAAATTCAGAAATG 847
Db 721 CTGTCCAGTTTATTTTTTTATGTTTATCTCGATGTATCAAAAAATTCAGAAATG 662
QY 848 ATCTCTGTAGATATCTGTTTATTTTGTGTCATCTTTAGAGTTATCAGGAATGTGTTA 907
Db 661 ATCTCTGTAGATATCTGTTTATTTTGTGTCATCTTTAGAGTTATCAGGAATGTGTTA 602
QY 908 AAACAAGAGAGAACTTTTCTAAGGAATGATACATAGAAAAGATTTTATTTTAAATGAG 967
Db 601 AAACAAGAGAGAACTTTTCTAAGGAATGATACATAGAAAAGATTTTATTTTAAATGAG 542
QY 968 TTGTAAAGCTGTGTTTCTTTGTGTCGAAGCTATCTGCCCAAGTTTATGCAAAATGGAC 1027
Db 541 TTGTAAAGCTGTGTTTCTTTGTGTCGAAGCTATCTGCCCAAGTTTATGCAAAATGGAC 482
QY 1028 ACATTTTTTATGTCAGAAAAACACACACACACACACACACACACACACACACACAC 1087
Db 481 ACATTTTTTATGTCAGAAAAACACACACACACACACACACACACACACACACACAC 422
QY 1088 AAAAAAAAAAAAAAAAAA 1104
Db 421 ACGAAAAACAAAGAAA 405
```

RESULT 10
ADN04817/c
ID ADN04817 standard; cDNA; 1321 BP.
XX
AC ADN04817;

```
XX 01-JUL-2004 (first entry)
DT Antipsoriatic cDNA sequence #623.
DE ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
KW Homo sapiens.
OS WO2004028479-A2.
XX 08-APR-2004.
PD 25-SEP-2003; 2003WO-US030907.
PF 25-SEP-2002; 2002US-0414006P.
PR (GETH ) GENENTECH INC.
XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;
XX WPI; 2004-305105/28.
DR P-PSDB; ADN04818.
XX New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX Claim 1; SEQ ID NO 1211; 3069pp; English.
XX The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polynucleotides of the invention.
XX Sequence 1321 BP; 414 A; 255 C; 236 G; 416 T; 0 U; 0 Other;
SQ
Query Match 57.3%; Score 632.6; DB 12; Length 1321;
Best Local Similarity 89.0%; Pred. No. 2.3e-121;
Matches 816; Conservative 0; Mismatches 69; Indels 32; Gaps 11;
QY 220 CCAAGCTGGCCGACATCGCGGAGCAGAGCGGGTGTATTGAAGATGATAGGATTGATG 279
Db 1321 CCAAGCTGGCCGACATCGCGGAGCAGAGCGGGTGTATTGAAGATGATAGGATTGATG 1262
QY 280 ACGTGTGAAAAATATGACGCGACAGGCACCT-CTGGTGTCTAACT-CCCAAGACAAT 337
Db 1261 ACGTGTGAAAAATATGACGCGACAGGCACCTCTGTGTCTAACTCTCCCAAGACAAT 1202
QY 338 GAGTTAAGGAGAGAAATAGGAACGGCGGTAAACAGTTATTGGCAAAAAGCATGAAAAGAGA 397
Db 1201 GAGTTAAGGAGAGAAATAGGAACGGCGGTAAACAGTTATTGGCAAAAAGCATGAAAAGAGA 1142
QY 398 AAGCACTTTGAAATTTATTACTAGCTTG-TACCCAGATGAATCAACACCTGTATCTG 456
Db 1141 AAGCACTTTGAAATTTATTACTAGCTTG-TACCCAGATGAATCAACACCTGTATCTG 1082
QY 457 GTAT-ATGCCCGGAGACAGATTAGGCGA-AGGAGGAGAGAGAGAGAAAGGCTTGGG 514
Db 1081 GTATCAGCGCGGAGACAGATTAGGCGA-AGGAGGAGAGAGAGAGAAAGGCTTGGG 1022
QY 515 C-CCTCTACAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 566
Db 1021 CTCCTCTGCAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 962
QY 567 -----TCCCATATAGAAATAAAGAGTCTCAGT-----GCAGTATTGGCAAAATTA 613
Db 961 TATATACATATATAAAGAAATAAAGAAAGTCTCAGTTCGACGATATTTCGCAAAATTAAT 902
QY 614 ATCCATTCTCTTTTAATACGGG----AATATTGGCATTATAGATCTGGATTTTG-ACCAC 668
Db 901 ATCCATTCTCTTTATACGGGTGATATTGGCATTATAGATCTGGATTTTG-ACCAC 842
QY 669 TTAATGAAGCGG-ACCACAGGTTTGGAGTGTGGCATCTTCGCTGATTTGGCTGT 727
Db 841 TTAATGAAGCGGCAACACAGGTTTGGAGTGTGGCATCTTCGCTGATTTGGCTGT 782
QY 728 TCCCAATGTTTACATTTTAACTCTGCAAAATGTTCTGTGCACTTGGATGTGAATG 787
Db 781 TCCCAATGTTTACATTTTAACTCTGCAAAATGTTCTGTGCACTTGGATGTGAATG 722
QY 788 CTGTCCAGTTTATTTTTTTATGTTTATCTCGATGTATCAAAAAATTCAGAAATG 847
Db 721 CTGTCCAGTTTATTTTTTTATGTTTATCTCGATGTATCAAAAAATTCAGAAATG 662
QY 848 ATCTCTGTAGATATCTGTTTATTTTGTGTCATCTTTAGAGTTATCAGGAATGTGTTA 907
Db 661 ATCTCTGTAGATATCTGTTTATTTTGTGTCATCTTTAGAGTTATCAGGAATGTGTTA 602
QY 908 AAACAAGAGAGAACTTTTCTAAGGAATGATACATAGAAAAGATTTTATTTTAAATGAG 967
Db 601 AAACAAGAGAGAACTTTTCTAAGGAATGATACATAGAAAAGATTTTATTTTAAATGAG 542
QY 968 TTGTAAAGCTGTGTTTCTTTGTGTCGAAGCTATCTGCCCAAGTTTATGCAAAATGGAC 1027
Db 541 TTGTAAAGCTGTGTTTCTTTGTGTCGAAGCTATCTGCCCAAGTTTATGCAAAATGGAC 482
QY 1028 ACATTTTTTATGTCAGAAAAACACACACACACACACACACACACACACACACACAC 1087
Db 481 ACATTTTTTATGTCAGAAAAACACACACACACACACACACACACACACACACACAC 422
QY 1088 AAAAAAAAAAAAAAAAAA 1104
Db 421 ACGAAAAACAAAGAAA 405
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QY 1088 AAAAAAAAAAAAAAAAAA 1104
 DB 901 ACAGAAACAAAGAAA 917

RESULT 12
 AAD31053
 ID AAD31053 standard; DNA; 3189 BP.
 XX
 AC AAD31053;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human PAPAP gene.
 XX
 KW Human; PAPAP protein; schizophrenia candidate gene; g34872 gene;
 KW schizophrenia; bipolar disorder; central nervous system disorder;
 KW psychotic disorder; mood disorder; autism; mental retardation;
 KW psychiatric disease; anxiety disorder; impulse-control disorder;
 KW eating disorder; cognitive disorder; personality disorder; vaccine;
 KW chromosome 1p35-p36; neuroleptic; antialcoholic; tranquiliser;
 KW antidepressant; nootropic; antiaddictive; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200212279-A2.
 XX
 XX 14-FEB-2002.
 XX
 XX 26-JUL-2001; 2001WO-1B001891.
 XX
 XX 07-AUG-2000; 2000US-0223482P.
 XX
 XX (GEST) GENSET.
 XX
 XX Bihain B, Bour B, Bougueleret L;
 XX
 XX WPI; 2002-241732/29.
 XX
 XX Novel isolated and purified or recombinant polynucleotide encoding PAPAP
 XX protein, useful for diagnosing and treating schizophrenia, bipolar
 XX disorder and other central nervous system disorders.
 XX
 XX Disclosure; Page 93-94; 96pp; English.
 XX
 XX The invention relates to human PAPAP polypeptides and polynucleotides.
 XX The invention also concerns the interaction of PAPAP with schizophrenia
 XX candidate gene g34872. PAPAP polypeptides, gene and anti-PAPAP antibodies
 XX are useful for treating schizophrenia, bipolar disorder or related
 XX central nervous system (CNS) disorders e.g. psychotic disorders, mood
 XX disorders, autism, substance dependence and alcoholism, mental
 XX retardation and other psychiatric diseases including cognitive, anxiety,
 XX eating, impulse-control and personality disorders. They are also used in
 XX vaccines. The present sequence is human PAPAP gene located on chromosome
 XX 1p35-p36
 XX
 XX Sequence 3189 BP; 691 A; 911 C; 959 G; 628 T; 0 U; 0 Other;
 XX

Query Match 55.0%; Score 607.2; DB 6; Length 3189;
 Best Local Similarity 89.2%; Pred. No. 5.6e-116;
 Matches 787; Conservative 0; Mismatches 63; Indels 32; Gaps 11;

QY 252 GTTGTATTGAGATGATAGGATTGATGACGTGCTGAAATAATGACCGACAAAGGCACCT 311
 DB 2158 GTTGTATTGAGATGATAGGATTGATGACGTGCTGAAATAATGACCGACAAAGGCACCT 2217

QY 312 -CTGGTGTCTAACT-CCCAAGACAAATGAGTTAAGGGAGAGAAATAGGAACCGCGGTAAAC 369
 DB 2218 CTGGTGTCTAACTCTCCCCAGACAAATGAGTTAAGGGAGAGAAATAGGAACCGCGGTAAAC 2277

QY 370 AGTTATTGCAAAACATGAAAGAGAAAGCACCTTTGAAATTTATTACTAGCTTG-TAC 428

DB 2278 AGTTATTGCAAAACATGAAAGAGAAAGCACCTTTGAAATTTATTACTAGCTTGCTAC 2337
 QY 429 CCACGATGAATCAACACCTGTATCTGGTAT-ATGCCCGGAGACAGATTAGGCCA-AGG 486
 DB 2338 CCACGATGAATCAACACCTGTATCTGGTATCAGGCCGGGAGACAGATTAGGCCAGAGG 2397
 QY 487 AGGAAGAGAGAGAGAGAAAGGCTTTGGGC-CCTCTACAAATAAAATAAAAAAATAATTT 545
 DB 2398 AGGAGGAGGAGGAGGAGGAGGCTCTGGGCTCTCTGCAAAATAAAATAAAAAATAATAA 2457
 QY 546 TAAATAATAAAATCCCTATA-----TCCCATATAAGAAATAAAAGAGTC 589
 DB 2458 TAAATAATAAAATAAAATAAAATTCATATATACATATAAAAGAAATAAAAGAGTC 2517
 QY 590 TCAGT----GCAGTATTGCGCAAAATTAATCCATTTCTTTTAAACCGG----AATATT 641
 DB 2518 TCAGTTGCGAGCTATTGTCAAAATTAATCCATTTCTTTTAAATACCGGGAATATTGC 2577
 QY 642 GGCATTATAGATCTGGAATTTTG-ACCACTTAATGAAGCGGC-ACCCAGGTGTTTGGAGG 699
 DB 2578 GCATTATAGATCTGGAATTTTGAACCACTTAATGAAGCGGCACACACAGGTGTTTGGAGG 2637
 QY 700 TGTGGCATCTCTGCTGATTTGGCTGTTCCCAATGTTTACATTATTAACTTGCACAAA 759
 DB 2638 TGTGGCATCTCTGCTGATTTGGCTGTTCCCAATGTTTACATTATTAACTTGCACAAA 2697
 QY 760 ATGTTCTCTGCTGACCTTGGATGTAATGCTGTCAGATTTTATTTTATTTTATGTTGTTATC 819
 DB 2698 ATGTTCTCTGCTGACCTTGGATGTAATGCTGTCAGATTTTATTTTATTTTATGTTGTTATC 2757
 QY 820 CTTGGATGTACAAAAAATTCAGAAATGATCTCTGTAGATATCTGTTTTTATTTTGTGTCAC 879
 DB 2758 CTTGGATGTACAAAAAATTCAGAAATGATCTCTGTAGATATCTGTTTTTATTTTGTGTCAC 2817
 QY 880 TCTTTAGAGTTATCAGGAATGTGTTTAAACAAGAGAGAACTTTCTAAGGAATGATA 939
 DB 2818 TCTTTAGAGTTATCAGGAATGTGTTTAAACAAGAGAGAACTTTCTAAGGAATGATA 2877
 QY 940 CATAGAAAAGATTTTATTTTAAATGAGTTCTGAAGCTTGTTTCTTTGTTGCTGCAAG 999
 DB 2878 CATAGAAAAGATTTTATTTTAAATGAGTTCTGAAGCTTGTTTCTTTGTTGCTGCAAG 2937
 QY 1000 CTATCTGCCCAAGTTAATGCAATGGAACACATTTTATGTGAGAAAAACACACACACAC 1059
 DB 2938 CTATCTGCCCAAGTTAATGCAATGGAACACATTTTATGTGAGAAAAACACACACACAC 2997
 QY 1060 AC 1101
 DB 2998 AC 3039

RESULT 13
 ABQ60975
 ID ABQ60975 standard; cDNA; 873 BP.
 XX
 AC ABQ60975;
 XX
 DT 26-FEB-2003 (first entry)
 XX
 DE PRO1489 protein encoding sequence.
 XX
 KW Neuroprotective; immunomodulator; cancer; chromosome 1; cytostatic;
 KW anti-inflammatory; gene therapy; nutritional supplement; wound; burn;
 KW ulcer; Alzheimer's disease; Huntington's disease;
 KW amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
 KW vulnery; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200231111-A2.
 XX
 XX 18-APR-2002.
 XX

PF 11-OCT-2001; 2001WO-US027760.
XX 12-OCT-2000; 2000US-00687527.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX N-PSDB; ABP43731.
DR WPI; 2002-426278/45.
XX N-PSDB; ABP43731.
XX New polypeptides and their encoded proteins, useful as nutritional
PT sources or supplements, or in gene therapy, particularly for treating
PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
PT inflammation.
XX Claim 1; SEQ ID # 188; 357pp + Sequence Listing; English.
XX The invention relates to 446 newly isolated polynucleotide sequences. The
CC activity of polynucleotides of the invention may be described as,
CC vulnerability, neuroprotective, immunomodulator, cytostatic and anti-
CC inflammatory. Compositions comprising nucleic acids of the invention are
CC useful for treating a mammalian subject, or as nutritional sources or
CC supplements. These are useful in gene therapy, particularly for treating
CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or
CC inflammation. The nucleic acids and polypeptides are also useful in
CC diagnostic and research methods. The sequences given in records ABQ60788-
CC ABQ1233 represent polynucleotides of the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 873 BP; 304 A; 144 C; 174 G; 251 T; 0 U; 0 Other;
Query Match 47.1%; Score 519.8; DB 6; Length 873;
Best Local Similarity 88.2%; Pred. No. 5.1e-98;
Matches 721; Conservative 0; Mismatches 62; Indels 34; Gaps 13;
QY 299 GCACGAGGACCTCTGGTGTCTAACT-CCCCAAGACAAATGAGTTAAGGGAGAGAAATAG 356
DB 53 GCACGAGGACCTCTGGTGTCTAACTCCCCAAGACAAATGAGTTAAGGGAGAGAAATAG 112
QY 357 GAACGGCGGTACAGTTATTGGCAAAAGCATGAAAGAGAGACATTTGAAATTTATT 416
DB 113 GAACGGCGGTACAGTTATTGGCAAAAGCATGAAAGAGAGACATTTGAAATTTATT 172
QY 417 ACTAGCTTG-TACCCACGATGAAATCAACACCTGTATCTGTAT-ATGCCCGGAGACAG 474
DB 173 ACTAGCTTGCTACCCACGATGAAATCAACACCTGTATCTGTATCAGCGCGGAGACAG 232
QY 475 ATTAGCGGA-AGGAGGAG 532
DB 233 ATGAGCGGAG 292
QY 533 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 576
DB 293 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 352
QY 577 GAATAAAGAGTCTCAGT----GCAGTATGGCAAAATTAATCCATTTCTTTTAAATAC 632
DB 353 ATAAAAAGAGTCTCAGTGTGACGCTATTGTCAAAATTAATCCATTTCTTTTAAATAC 412
QY 633 GGG----ATATGTGCATTTATAGATCTGGATTTTG-ACCACCTAATGAGCGGC-ACCC 686
DB 413 CGGTGAATATTGCGCAATTTATAGATCTGGATTTTGAAACCACTTAATGAGCGGCACACC 472
QY 687 AGGTGTTTTAGGTGTTGCTATTCTTGGCTGATTTTGGCTGTTTCCCAATGTTTACATTTAT 746
DB 473 AGGTGTTTTAGGTGTTGCTATTCTTGGCTGATTTTGGCTGTTTCCCAATGTTTACATTTAT 532
QY 747 TAATCTGCAAAATAGTGTCTGTCACCTTGGATGTGAAATGCTGTCAGTGTTCATTTTTT 806

DB 533 TAATCTGCAAAATAGTGTCTGTCACCTTGGATGTGAAATGCTGTCAGTGTTCATTTTT 592
QY 807 TTATGTTTGTATCTTGGATGTACAAAAATTCAGAAAAATGATCTCTGTAGATATTTCTGT 866
DB 593 TTATGTTTGTATCTTGGATGTACAAAAATTCAGAAAAATGATCTCTGTAGATATTTCTGT 652
QY 867 TTTATTTGGTCACTCTTTAGAAAGTTATCAGGAATGTGTTTAAAAACAAGAGAACTTTT 926
DB 653 TTTATTTGGTCACTCTTTAGAAAGTTATCAGGAATGTGTTTAAAAACAAGAGAACTTTT 712
QY 927 CTAAGGAATG-ATACATAG-AAAAATTTTATTTTAAAAATGAGTTGTTAAAGCTGTGTTT 984
DB 713 CTAAGGAATGATACATAGCAAAAGATTTTATTTTAAAAATGAGTTGTTAAAGCTGTGTTT 772
QY 985 CTTTGTCTGCAAGCTATCTGCCCAAGTTAATGCAAAATGACACATTTTTTTATGTCAGA 1044
DB 773 CTTTGTCTGCAAGCTATCTGCCCAAGTTAATGCAAAATGACACATTTTTTTATGTCAGA 832
QY 1045 AAAAC 1081
DB 833 AAAAC 869
RESULT 14
ABX97604
ID ABX97604 standard; cDNA; 553 BP.
AC ABX97604;
XX
DT 16-MAY-2003 (first entry)
XX
DE cDNA encoding novel human protein NOV9a.
XX Human; NOV; adrenoleukodystrophy; congenital adrenal hyperplasia;
KW haemophilia; hypercoagulation; autoimmune disease; allergy;
KW immunodeficiency; transplantation; Von Hippel-Lindau syndrome;
KW Alzheimer's disease; stroke; tuberculous sclerosis; hypercalcaemia;
KW Parkinson's disease; Huntington's disease; cancer; fertility; diabetes;
KW adult respiratory distress syndrome; infection; tissue typing;
XX
XX Homo sapiens.
XX WO200290500-A2.
XX PD 14-NOV-2002.
XX PF 02-MAY-2002; 2002WO-US014256.
XX
XX 03-MAY-2001; 2001US-0288395P.
PR 07-MAY-2001; 2001US-0289087P.
PR 08-MAY-2001; 2001US-0289619P.
PR 09-MAY-2001; 2001US-0289817P.
PR 09-MAY-2001; 2001US-0289818P.
PR 11-MAY-2001; 2001US-0290194P.
PR 14-MAY-2001; 2001US-0290753P.
PR 15-MAY-2001; 2001US-0291189P.
PR 21-MAY-2001; 2001US-0292374P.
PR 23-MAY-2001; 2001US-0293107P.
PR 25-MAY-2001; 2001US-0293747P.
PR 29-MAY-2001; 2001US-0294110P.
PR 30-MAY-2001; 2001US-0294434P.
PR 10-SEP-2001; 2001US-0318346P.
PR 17-SEP-2001; 2001US-0322646P.
PR 01-MAY-2002; 2002US-00136728.
XX
XX (CURA-) CURAGEN CORP.
XX Spytek KA, Li L, Edinger SR, Stone DJ, Guo X, Anderson DW;
PI Patturajan M, Gerlach VL, Taupier RJ, Pena CE, Padigar M;
PI Kekuda R, Gorman L, Zerhusen BD, Smithson G, Macdougall JR;
PI Mezes PS, Peyman JA, Zhong M;

XX WPI; 2003-103511/09.
DR P-PSDB; ABU65229.
XX
XX New NOVX polypeptides and polynucleotides useful for treating or
PT preventing e.g. congenital adrenal hyperplasia, hemophilia,
PT hypercoagulation, autoimmune disease, allergies, immunodeficiencies,
PT transplantation.
XX
XX Claim 1; Page 106-107; 300pp; English.
XX
XX The invention describes an isolated polypeptide, NOVX, comprising a
CC sequence or a mature form of one of 21 51-1543 residue amino acid
CC sequences (P1-P21), given in the specification. The NOVX polypeptides,
CC polynucleotides and antibodies are useful in the manufacture of a
CC medicament for treating or preventing e.g. adrenoleukodystrophy,
CC congenital adrenal hyperplasia, haemophilia, hypercoagulation, autoimmune
CC disease, allergies, immunodeficiencies, transplantation, Von Hippel-
CC Lindau syndrome, Alzheimer's disease, stroke, tuberculous sclerosis,
CC hypercalcaemia, Parkinson's disease, Huntington's disease, cancer,
CC fertility, diabetes, adult respiratory distress syndrome, viral,
CC bacterial and parasitic infections. The nucleic acid sequences may be
CC used in chromosome mapping, identifying individual from minute biological
CC samples (tissue typing), and in forensic identification of a biological
CC sample. This sequence encodes a novel human protein (NOV)
XX
XX Sequence 553 BP; 169 A; 133 C; 170 G; 81 T; 0 U; 0 Other;
SQ
Query Match 40.1%; Score 443.2; DB 8; Length 553;
Best Local Similarity 94.0%; Pred. No. 3.4e-82;
Matches 515; Conservative 0; Mismatches 28; Indels 5; Gaps 5;
QY 16 CGCTGACCTCTGTCGGCGGGCGGAGCGCGGGCGGAGGCGCGCGGCGGAGCCCG 75
DB 1 CGCTGACCTCTGTCGGCGGGCGGAGCGCGGGCGGAGGCGCGCGGCGGAGCCCG 60
QY 76 CGAGCGGACCATGTGGAGGTGCTGCCCTACGGCGACGAGAGCTGAGCCCTACGGCG 135
DB 61 CGGACGCGACCATGTGGAGGTGCTGCCCTACGGCGACGAGAGCTGAGCCCTACGGCG 120
QY 136 ACGGCGGCGAGCGGGCGGAGATCTCTCTGCGCGCTGAGGACGACACCACTCTTCG 195
DB 121 ACGGCGGCGAGCTGGGCGGAGATCTCTCTGCGCGCTGAGGACGACACCACTCTTCG 180
QY 196 GCSCCGGCGAGAACAGCGGCGGCCCAAGCTGGGCGGAGATCGCGCGGAGCAAGCGGTTG 255
DB 181 GCSCCGGCGAGAACAGCGGCGGCCCAAGCTGGGCGGAGATCGCGCGGAGCAAGCGGTTG 240
QY 256 TTATTGAAGATGATAGATTGATGACGTGCTGAAAATATGACCGAAGGCACTTCTG 314
DB 241 TTATTGAAGATGATAGATTGATGACGTGCTGAAAATATGACCGAAGGCACTTCTG 300
QY 315 GTGCTTAACCT-CCCCAAGACATGATGTTAAGGGAGAGATAGGAACGCGGTAAAGTT 373
DB 301 GTGCTTAACCTCCCCAAGACATGATGTTAAGGGAGAGATAGGAACGCGGTAAAGTT 360
QY 374 ATTGGCAAAAGCATGAAAGAGAAAGCACTTTGAAAATTTATTACTAGCTTG-TACCCAC 432
DB 361 ATTGGCAAAAGCATGAAAGAGAAAGCACTTTGAAAATTTATTACTAGCTTCTACCCAC 420
QY 433 GATGAATCAACACTGTATCTGGTAT-ATGCCCCGAGACAGATAGGCGA-AGAGGA 490
DB 421 GATGAATCAACACTGTATCTGGTATCAGGCGCGGAGACAGATGAGGCGAGAGGGA 480
QY 491 AGAGAGAGAGAGAAAGGCTTGGGCCCTCTACAAATAAAATAAAAAAAATTTAAAA 550
DB 481 GGAGGAGGAGGAGAGGCTTGGGGCTCTCTGCAAAAAAATAAAAAAATAAAAAA 540
QY 551 TAAATAAA 558
DB 541 AAAAAAAA 548

RESULT 15
AAC06588
ID AAC06588 standard; cDNA; 524 BP.
XX
AC AAC06588;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 10663.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-00200610.
XX
XX 26-FEB-1999; 99US-0122487P.
XX
XX (GEST) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX WPI; 2000-500381/45.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
XX Claim 1; SEQ ID NO 10663; 71pp + Sequence Listing; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors
XX
XX Sequence 524 BP; 159 A; 86 C; 93 G; 179 T; 0 U; 7 Other;
SQ
Query Match 38.7%; Score 427.2; DB 3; Length 524;
Best Local Similarity 97.8%; Pred. No. 7e-79;
Matches 451; Conservative 2; Mismatches 6; Indels 2; Gaps 2;
QY 645 ATTATAGATCTCGATTTTG-ACCATTAAATGAAGCGGC-ACCCAGGTGTTTTCAGGTGT 702
DB 24 ATTATAGATCTCGATTTTGACCACTTAATGAAGCGGCACACCGGTGTTTCAGGTGT 83
QY 703 TGGCATTTCTCGCTGATTTGGCTGTTCCCAATGTTTACATTTAATCTTGCAAAATG 762
DB 84 TGGCATTTCTCGCTGATTTGGCTGTTCCCAATGTTTACATTTAATCTTGCAAAATG 143
QY 763 GTTCTGTGCACCTCGGATGTAATGCTGTCAGTTTATTTTATTTTATTTGTTATCTCT 822
DB 144 GTTCTGTGCACCTCGGATGTAATGCTGTCAGTTTATTTTATTTTATTTGTTATCTCT 203
QY 823 GGATGTACAAAAATTCAGAAAAATGATCTCTGTAGATATTCTGTTTATTTTGTGTCATCT 882
DB 204 GGATGTACAAAAATTCAGAAAAATGATCTCTGTAGATATTCTGTTTATTTTGTGTCATCT 263
QY 883 TTAGAAGTTATCAGGATGTTTAAACACAGAGAGAACTTTTCTAAGGATATACAT 942

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Db 264 TTAGAAAGTTATCAGGAATGTGTTTAAAAACAGAGAGAGAACTTTTCTAAGGAATGATACAT 323
Qy 943 AGAAAAGATTTTATTTTAAATGAGTGTGTAAGCTTGTGTTTCTTTTGTGCTGCAAGCTA 1002
Db 324 AGAAAAGATTTTATTTTAAATGAGTGTGTAAGCTTGTGTTTCTTTTGTGCTGCAAGCTA 383
Qy 1003 TCTGCCCAAGTTAATGCAAAATGGACACACATTTTTTTATGTCAGAAAAACACACACACACA 1062
Db 384 TCTGCCCAAGTTAATGCAAAATGGACACACATTTTTTTATGTCAGAAAAACACACACACACA 443
Qy 1063 CACACACACACACACACACGAAAAAAGAAAAA 1103
Db 444 CACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC 484
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Search completed: March 30, 2005, 00:47:34
Job time : 643 secs

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Result No.	Score	Query		DB	ID	Description
		Match	%			
1	803.8	72.8	1876	4	US-09-566-921-70	Sequence 70, Appl
2	790	71.6	1581	3	US-09-513-300-1	Sequence 1, Appl
3	427.2	38.7	524	4	US-09-513-999C-10663	Sequence 10663, Appl
C 4	270	24.5	417	4	US-09-702-705-475	Sequence 475, Appl
C 5	270	24.5	417	4	US-09-736-457-475	Sequence 475, Appl
C 6	270	24.5	417	4	US-09-614-1248-475	Sequence 475, Appl
C 7	270	24.5	417	4	US-09-671-325-475	Sequence 475, Appl
C 8	270	24.5	417	4	US-09-589-184-475	Sequence 475, Appl
C 9	270	24.5	417	4	US-09-658-824-475	Sequence 475, Appl
C 10	165	14.9	336	4	US-09-654-133-560	Sequence 560, Appl
11	155.8	14.1	183	4	US-09-513-999C-10536	Sequence 10536, Appl
12	118.6	10.7	1045	3	US-09-313-300-9	Sequence 9, Appl
13	96.4	8.7	315	4	US-09-621-976-15158	Sequence 15158, Appl
14	94	8.5	90	4	US-09-513-999C-29981	Sequence 29981, Appl
15	77.6	7.0	90	4	US-09-513-999C-24816	Sequence 24816, Appl
C 16	67.2	6.1	7218	1	US-08-232-463-14	Sequence 14, Appl
C 17	60.2	5.5	11509	4	US-09-949-016-17379	Sequence 17379, Appl
C 18	58.2	5.3	601	4	US-09-949-016-48404	Sequence 48404, Appl
C 19	58	5.3	92139	4	US-09-918-686-1	Sequence 1, Appl
C 20	57.6	5.2	601	4	US-09-949-016-129237	Sequence 129237, Appl
C 21	57.6	5.2	98864	4	US-09-949-016-15403	Sequence 15403, Appl
C 22	57.6	5.2	114842	4	US-09-949-016-14993	Sequence 14993, Appl
C 23	56.8	5.1	360470	4	US-09-949-016-13173	Sequence 13173, Appl
C 24	56.4	5.1	601	4	US-09-949-016-48403	Sequence 48403, Appl
C 25	56	5.1	102304	4	US-09-949-016-12589	Sequence 12589, Appl
C 26	55.6	5.0	28129	4	US-09-949-016-17168	Sequence 17168, Appl
C 27	55.6	5.0	28129	4	US-09-949-016-17169	Sequence 17169, Appl

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QY 310 CT-CTGGTGTCTAACT-CCCAAGACAAATGAGTTAAGGAGAGAAATAGGAACGGCGGTA 367
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QY 578 CTCTGGTGTCTAACTCCCAAGACAAATGAGTTAAGGAGAGAAATAGGAACGGCGGTA 637
Db |||
QY 368 ACAGTTATTGGCAAAAGCATGAAAGAGAGAAACACTTTGAAATTTATTACTAGCTTG-T 426
Db |||
QY 638 ACAGTTATTGGCAAAAGCATGAAAGAGAGAAACACTTTGAAATTTATTACTAGCTTGCT 697
Db |||
QY 427 ACCCAGCATGAATCAACACCTGTATCTGGTAT-ATGCCCGGAGACAGATTAGGCGAAG 485
Db |||
QY 698 ACCCAGCATGAATCAACACCTGTATCTGGTATCTGGTATCTGGTATCTGGTATCTGGT 757
Db |||
QY 486 GAGCAAGAGAGAGAGAGAAAGCTTGGCCCTCTACAAATAAATAAATAAATAAATAAAT 545
Db |||
QY 758 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 817
Db |||
QY 546 TAAATAAAT- 545
Db |||
QY 818 AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 877
Db |||
QY 587 GTCTCAGT- 545
Db |||
QY 878 GTCTCAGTGTGACGCTATTTGTCAAAATTAATATCCATTTCTTTTATATACGGTGATAT 937
Db |||
QY 641 --TGCCATTATAGATCTGGATTTTG-ACCACCTTAATGAAGCGGC-ACCCAGAGTGTG 696
Db |||
QY 938 TGCGCAATTATAGATCTGGATTTTGAAACCACTTAATGAAGCGGCACACAGGTGTTTG 997
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QY 697 AGGTGTGGCATTTCTCGCTGATTTGGCTGTTCCCAATGTTTACATTTAATCTTGCA 756
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QY 998 AGGTGTGGCATTTCTCGCTGATTTGGCTGTTCCCAATGTTTACATTTAATCTTGCA 1057
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QY 757 AAAATGTTCTGTCGACTTGGATGTCGAATGCTGCCAGTGTATTTTATTTATCTGTT 816
Db |||
QY 1058 AAAATGTTCTGTCGACTTGGATGTCGAATGCTGCCAGTGTATTTTATTTTATGTTGT 1117
Db |||
QY 817 ATCTTTGGATGTACAAAAAATTCAGAAAAATGATCTCTGTAGATATTTCTGTTTATTTGG 876
Db |||
QY 1118 ATCTTTGGATGTACAAAAAATTCAGAAAAATGATCTCTGTAGATATTTCTGTTTATTTGG 1177
Db |||
QY 877 TCATCTTTAGAGTTATCAGGAATGTTTAAACCAAGAGAGAACTTTTCTAAGGAATG 936
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QY 1178 TCATCTTTAGAGTTATCAGGAATGTTTAAACCAAGAGAGAACTTTTCTAAGGAATG 1237
Db |||
QY 937 ATACATAGAAAGATTTTATTTTAAATCAGTTGTAAGCTTGTGTTCTTTGTTGCTGC 996
Db |||
QY 1238 ATACATAGAAAGATTTTATTTTAAATCAGTTGTAAGCTTGTGTTCTTTGTTGCTGC 1297
Db |||
QY 997 AAGCTATCTGCCAAGTTAATGCAATGGACACATTTTATGTCAGAAAAACACACACA 1056
Db |||
QY 1298 AAGCTATCTGCCAAGTTAATGCAATGGACACATTTTATGTCAGAAAAACACACACA 1357
Db |||
QY 1057 CACACACACACACACACACACACACACACACACACACACACACACACACACACAC 1104
Db |||
QY 1358 CANGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1405
Db |||
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RESULT 2

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US-09-313-300-1
; Sequence 1, Application US/09313300
; Patent No. 6222027
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew, R.
; APPLICANT: Lal, Preeti
; APPLICANT: Yue, Henry
; APPLICANT: Tang, Tom, Y.
; APPLICANT: Baughn, Mariah, R.
; APPLICANT: Azimzai, Yalda
; TITLE OF INVENTION: MOLECULES EXPRESSED IN HIPPOCAMPUS
; FILE REFERENCE: PB-0012 US
; CURRENT APPLICATION NUMBER: US/09/313,300
; CURRENT FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 15
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; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 1581
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY:
; OTHER INFORMATION: 239240
; PUBLICATION INFORMATION:
US-09-313-300-1

Query Match 71.6%; Score 790; DB 3; Length 1581;
Best Local Similarity 90.5%; Pred. No. 6.5e-177; Indels 33; Gaps 12;
Matches 985; Conservative 0; Mismatches 70;

QY 48 GCGGAGAGAGCGCGCGCGGAGCCCGCGGACGCGGCGGAGAGAGAGAGAGAGAGAGAGAG 107
Db 1 GCGGAGAGAGCGCGCGCGGAG-CCCGGACGCGGAG-CCCGGAGAGAGAGAGAGAGAGAGAG 59
QY 108 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 167
Db 60 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 119
QY 168 GCGCTGCAGGACACCAACAACTTCTCGCGCGCGGCGGAGAGAGAGAGAGAGAGAGAGAG 227
Db 120 GCGCTGCAGGACACCAACAACTTCTCGCGCGCGGCGGAGAGAGAGAGAGAGAGAGAGAG 179
QY 228 GCGCAGATCGCGCGGAGCAAGCGGTTGTTATTGAAGATAGATAGATAGATAGATAGATAG 287
Db 180 GCGCAGATCGCGCGGAGCAAGCGGTTGTTATTGAAGATAGATAGATAGATAGATAGATAG 239
QY 288 AAAAATATGACCGACACAGGCGACCT-CTGGTGTCTAACT-CCCCAAGAGCAATGAGTTAAG 345
Db 240 AAAAATATGACCGACACAGGCGACCTCTCTGTTCTAACTCCCCAAGAGCAATGAGTTAAG 299
QY 346 GAGAGAGATAGAAACGCGGTAACAGATTATTGGCAAAAGCATGAAAGAGAGAGAGAGAGAG 405
Db 300 GAGAGAGATAGAAACGCGGTAACAGATTATTGGCAAAAGCATGAAAGAGAGAGAGAGAGAG 359
QY 406 TGAATTTATTACTAGCTTG-TACCCAGATGAAATCAACACCTGTATCTGGTAT-ATG 463
Db 360 TGAATTTATTACTAGCTTG-TACCCAGATGAAATCAACACCTGTATCTGGTATCAGG 419
QY 464 CCCGAGACAGATTAGGCGA-AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 521
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QY 522 CAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 566
Db 480 CAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 539
QY 567 -TCCCATATAGATTAAGAGTCTCAGT-----GCAGTATGGCAAAATTAATATCCATTT 621
Db 540 CATATAAGAAATAAATAAAGAGTCTCAGTATTTGTCAGTATTTGTCAGTATTTGTCAGTAT 599
QY 622 CTTTTTAATACGGG- ---AATATTGGCATATAGATCTGGATTTTG-ACCACTTAATGAA 676
Db 600 CTTTTTAATACGGTGAATATTGGCAATTAAGATCTGGATTTTGAAACCACTTAATGAA 659
QY 677 GCGGC-ACCCAGAGTGTGAGGTGTGGCATTTCTTGGCTGATTTGGCTGTGTTCCCAATG 735
Db 660 GCGGCAACACAGGTGTTTGAGGTGTGGCATTTCTTGGCTGATTTGCGTGTGTTGCTGTTCC 719
QY 736 TTTACATTTTATCTTGCAGAAATGTTCTGTCGACTTGGATGTCGAATGTCGTCAG 795
Db 720 TTTACATTTTATCTTGCAGAAATGTTCTGTCGACTTGGATGTCGAATGTCGTCAG 779
QY 796 TTTTATTTTATTTTATGTTTATCTTGGATGTCAGAAAAATTCAGAAAAATGATCTCTGT 855
Db 780 TTTTATTTTATTTTATGTTTATCTTGGATGTCAGAAAAATTCAGAAAAATGATCTCTGT 839
QY 856 AGATATCTGTTTATTTTGGTCTATCTTTAGAGATTAAGAGATGTTTAAACAGAA 915
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[illegible]

RESULT, T 3

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US-09-513-999C-10663
; Sequence 10663, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

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? PARENT NO. 0783961
? FILE REFERENCE: 59 US2.REG
? CURRENT APPLICATION NUMBER: US/09/513,999C
? CURRENT FILING DATE: 2000-02-24
? PRIOR APPLICATION NUMBER: US 60/122,487
? PRIOR FILING DATE: 1999-02-26
? NUMBER OF SEQ ID NOS: 35681
? SOFTWARE: Patent.pm
? SEQ ID NO 10663
? LENGTH: 524
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? TYPE: DNA
? ORGANISM: Homo sapiens
?
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: 465
? OTHER INFORMATION: r=a or g
?
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: 471
? OTHER INFORMATION: n=a, g=c or t

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US-09-513-999C-10663

Query Match 38.7%; Score 427.2; DB 4; Length 524;
Best Local Similarity 97.8%; Pred. No. 2.4e-91;
Matches 451; Conservative 2; Mismatches 6; Indels 2

645	Qy	ATTATAGATCTGATTTTG-ACACCTAATGAAGCGC-ACCCACGGTGTTTTGAGGTGT	702
24	Db	ATTATAGATCTGATTTTGAAACACCTAATGAAGCGGCAACACACAGGTGTTTTGAGGTGT	83
703	Qy	TGGCATTCTTCGCTGATTTTGGCTGTTCCTCAATGTTTACATTATTAACTTTGCAAAAATG	762
84	Db	TGGCATTCTTCGCTGATTTTGGCTGTTCCTCAATGTTTACATTATTAACTTTGCAAAAATG	143
763	Qy	GTTCTGTGCATCTGGATGTGAATATGCTGTCCAGTGTCTTTTATTTTTTATGTGTATTATCTT	822
144	Db	GTTCTGTGCATCTGGATGTGAATATGCTGTCCAGTGTCTTTTATTTTTTATGTGTATTATCTT	203
823	Qy	GGATGTACAAAAAATTCAGAAAAATGATCTCTGTAGATATTCTGTTTTTATTTTGGTCACT	882
204	Db	GGATGTACAAAAAATTCAGAAAAATGATCTCTGTAGATATTCTGTTTTTATTTTGGTCACT	263
883	Qy	TTAGAAGTTATCAGGAATGTGTTTAAAAACAAGAGAGAACTTTTCTAAGGAATGATACAT	942
264	Db	TTAGAAGTTATCAGGAATGTGTTTAAAAACAAGAGAGAACTTTTCTAAGGAATGATACAT	323
943	Qy	AGAAAGATTTTATTTTAAATCAGTTGTAAAGCTTGTGTTCTCTTGTGCTGCCAGCTA	1002
324	Db	AGAAAGATTTTATTTTAAATCAGTTGTAAAGCTTGTGTTCTCTTGTGCTGCCAGCTA	383
1003	Qy	TCTGCCCAAGTTAATGCAATGGACACATTTTTTATGTTCAGAAAAACACACACACACA	1062
384	Db	TCTGCCCAAGTTAATGCAATGGACACATTTTTTATGTTCAGAAAAACACACACACACA	443
1063	Qy	CACACACACACACACACACGAAAAAATAAAAAAATAAAAAA 1103	
444	Db	CACACACACACACACACACGCGAANAACAGAAAAAATAAAAA 484	

RESULT 4

US-09-702-705-475/c
; Sequence 475, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION.

1	GENERAL INFORMATION:
2	APPLICANT: Wang, Tongtong
3	APPLICANT: Bangur, Chaitanya S.
4	APPLICANT: Lodes, Michael A.
5	APPLICANT: Fanger, Gary
6	APPLICANT: Vedvick, Tom
7	APPLICANT: Carter, Darrick
8	APPLICANT: Retter, Marc
9	APPLICANT: Mannion, Jane

APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER

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; FILE OR INVENTOR: 210121.478C14
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/0
; CURRENT FILING DATE: 2000-10-30

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; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSEQ for Windows Version 3.0

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; SEQ ID NO 475
; LENGTH: 417
; TYPE: DNA

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; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C11
; CURRENT APPLICATION NUMBER: US/09/658,824
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 1788
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 475
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(417)
; OTHER INFORMATION: n = A,T,C or G
US-09-658-824-475

Query Match      24.5%; Score 270; DB 4; Length 417;
Best Local Similarity 83.4%; Pred. No. 3.2e-54;
Matches 342; Conservative 0; Mismatches 62; Indels 6; Gaps 3;

QY 521 ACAATAAATAAAAAAATTTAAATAATAAAATCCCTATATCCCATATAGAAAT 580
Db 410 ATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAG 351
QY 581 AAAAGAGTCTCAGTCAGTATGGCAAAATTAATCAATCTCTTTTAATACGGG---A 636
Db 350 AGTCTCAGTTCAGCTATTTGTCAAAATTAATCAATCTCTTTTAATACGGGAAAT 291
QY 637 ATATTGGCATATATAGATCTGGATTTTG-ACCACCTTAATGAAGCGGCACC-CCAGGTGTTT 694
Db 290 ATTGGCAATATATAGATCTGGATTTTGAAACCACTTAATGAAGCGGCACCAGGTGTTT 231
QY 695 TGAGGTGTTGGCAATCTTCGCTGATTTGGCTGTTCCCAATGTTTACATTTAATCTTG 754
Db 230 TGAGGTGTTGGCAATCTTCGCTGATTTGGCTGTTCCCAATGTTTACATTTAATCTTG 171
QY 755 CAAAAATGGTTCGTGCACCTTGGATGGAATGCTGCTGCAATTTATTTTATGTTG 814
Db 170 CAAAAATGGTTCGTGCACCTTGGATGGAATGCTGCTGCAATTTATTTTATGTTG 111
QY 815 TTATCCTTGGATGACAAAATAATTCAGAAAATGATCTCTGTAGATATCTGTTTATTTT 874
Db 110 TTATCCTTGGATGACAAAATAATTCAGAAAATGATCTCTGTAGATATCTGTTTATTTT 51
QY 875 GGTCTCTTTAGAGTTATCAGGAATGTTTAAACAAAGAGAGAACTT 924
Db 50 GGTCTCTTTAGAGTTATCAGGAATGTTTAAACAAAGAGAGAACTT 1
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RESULT 10
US-09-854-133-560
; Sequence 560, Application US/09854133
; Patent No. 6759508
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 560
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(336)
; OTHER INFORMATION: n = A,T,C or G
US-09-854-133-560

Query Match      14.9%; Score 165; DB 4; Length 336;
Best Local Similarity 76.8%; Pred. No. 2e-29;
Matches 238; Conservative 0; Mismatches 66; Indels 2; Gaps 3;

QY 524 AATAAATAAAAAAATTTAAATAATAAAATCCCTATATCCCATATAAGAAATAAA 583
Db 27 AATAAATAAATAAATAAATAAATAAATTCACATATACACATATAAAGAAATAAAGAG 86
QY 584 AGAGTCTCAGTCAGTATTTGGCAAAATTAATCAATCTCTTTTAATACGGG---AATA 639
Db 87 TCTCAGTTGCAGCTATTTGTCAAAATTAATATCCATCTCTTTTATATACGGTGAATAT 146
QY 640 TTGGCATATATAGATCTGGATTTTG-ACCACCTTAATGAAGCGGCACC-CCAGGTGTTTGA 697
Db 147 GCGCAATATATAGATCTGGATTTTGAAACCACTTAATGAAGCGGCACCAGGTGTTTGA 206
QY 698 GGTGTGGCATTTCTCGCTGATTTGGCTGTTCCCAATGTTTACATTTATTTATCTTGCAA 757
Db 207 GGTGTGGCATTTCTCGCTGATTTGGCTGTTCCCAATGTTTACATTTATTTATCTTGCAA 266
QY 758 AAATGGTTCGTGCACCTTGGATGGAATGCTGCTGCAATTTATTTTATGTTGTTA 817
Db 267 AAATGGTTCGTGCACCTTGGATGGAATGCTGCTGCAATTTATTTTATGTTGTTA 326
QY 818 TCCTTGGATG 827
Db 327 TCCTTGGATG 336

RESULT 11
US-09-513-999C-10536
; Sequence 10536, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 10536
; LENGTH: 183
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-10536

Query Match      14.1%; Score 155.8; DB 4; Length 183;
Best Local Similarity 97.8%; Pred. No. 2.2e-27;
Matches 179; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 183 AACAACTTCTTCGGCGCGCGGCAGAACAAAGCGCGCGCCCAAGCTGGGCCAGATCGGCGG 242
Db 1 AACAACTTCTTCAGCGCGCGGCAGAACAAAGCGCGCGCCCAAGCTGGGCCAGATCGGCGG 60
QY 243 AGCAAGCGGGTGTATTGTAAGATGATGAGATTGATGACGTGTGCTGCTGCTGCTGCTGCTG 302
Db 61 AGCAAGCGGGTGTATTGTAAGATGATGAGATTGATGACGTGTGCTGCTGCTGCTGCTGCTG 120
QY 303 AAGGCACCT-CTGGTGTCTAACT-CCCCAAGACAATGAGTTAGGGAGAGATAGAGAC 360
Db 121 AAGGCACCTCTCTGTGTCTAACTCCCCAAGACAATGAGTTAGGGAGAGATAGAGAC 180
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Qy 361 GGC 363
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Db 181 GGC 183

RESULT 12

US-09-313-300-9
; Sequence 9, Application US/09313300
; Patent No. 6222027
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew, R.
; APPLICANT: Lal, Preeti
; APPLICANT: Yue, Henry
; APPLICANT: Tang, Tom, Y.
; APPLICANT: Baughn, Mariah, R.
; APPLICANT: Azimzai, Yalda
; TITLE OF INVENTION: MOLECULES EXPRESSED IN HIPPOCAMPUS
; FILE REFERENCE: PB-0012 US
; CURRENT APPLICATION NUMBER: US/09/313,300
; CURRENT FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PERL Program
; SEQ ID NO 9
; LENGTH: 1045
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (871)...(899)
; OTHER INFORMATION: a or g or c or t, unknown, or other
; NAME/KEY:
; OTHER INFORMATION: 700122146
; PUBLICATION INFORMATION:
US-09-313-300-9

Query Match 10.7%; Score 118.6; DB 3; Length 1045;
Best Local Similarity 62.1%; Pred. No. 3.2e-18;
Matches 259; Conservative 0; Mismatches 144; Indels 14; Gaps 4;
Qy 532 AAAAAAAAAAATTTAAATATAAATCCCTATATCCCATATAGATATAAGATGCTC 591
Db 2 AATAAATAAATAAATAAATCACTATATACACATATAAAGAAAAAAGTGTGAGTTGC 61
Qy 592 AGTCAGATTTGGCAAAATTAATCCATTCTTTTAAATACGGGAATAT--TGCCATTAT 649
Db 62 AGCTACTTGTGAAATTAATACCTGTTCTTTTATCTATGTAATATCGTGCATATAT 121
Qy 650 AGATCTGATTTTG--ACCACCTTAATGAAGCGGCACCCAGGTGTTTTCGAGGTGTTGGCAT 708
Db 122 AGATCTGATTTTGAACCACTTCTGAAAGCAGCAGCAGTACTCGAAGGTGTTGTGT 181
Qy 709 TCTTCGCTGATTTGGCTGTTCCCAATGTTTACATTAATTTTTCGAAAAAATGTTCTG 768
Db 182 TCTTCGCTGATTTGGCTGTTTCCCAATGTTTACATTAATTTTTCGAAAAAATGATCTG 241
Qy 769 TGCACTTCGATGTAAGTCTGTCAG--TTTATTTTATTTTATGTTGTTATCTTCT 822
Db 242 TGCACCTTGATGTGACATGCTGTCTAGTCCGGTTTCATCTTTTTTTTAAATGTTGTTAT 301
Qy 823 GGATGTACAAAAAATTCAGAAAAATGATCTCTGTAGATATCTGTTTATTTTGTGTCACT 882
Db 302 TTTTGGATGTACAAAAAATAATTTGGGGGAGGGGTGATCTCTGTAGATCTCTTGTAC 361
Qy 893 TTAGAGTTATC-----AGGAATGTTTAAACACAGAAAGAACTTTTCTTAAGAA 934
Db 362 TTTGAAGTTACCGGAATGGAACGGGTCTTAAAGCAGAAAGTAACTTTTTCGAAGAA 418

RESULT 13

US-09-621-976-15158
; Sequence 15158, Application US/09621976

; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15158
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-15158

Query Match 8.7%; Score 96.4; DB 4; Length 315;
Best Local Similarity 92.5%; Pred. No. 3.2e-13;
Matches 135; Conservative 0; Mismatches 6; Indels 5; Gaps 3;
Qy 252 GTTGTATTGAAGATGATAGGATTTGATGACGTGCTGAAAAATATGACCGACAAGGCACCT 311
Db 172 GTTGTATTGAAGATGATAGGATTTGATGACG---TGAATAATATGACCGACAAGGCACCT 228
Qy 312 -CTGCTGTCTAACT-CCCCAAAGACAATGAGTTTAAGGGAGAGAAATAGGAACGGCGGTAAC 369
Db 229 CCTGCTGTCTAACTCCCCAAAGACAATGAGTTTAAGGGAGAGAAATAGGAACGGCGGTAAC 288
Qy 370 AGTTATTGGCAAAAGCATGAAAAGA 395
Db 289 AGTTATTGGCAAAAGCATGAAAAGA 314

RESULT 14

US-09-513-999C-29981
; Sequence 29981, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 29981
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-29981

Query Match 8.5%; Score 94; DB 4; Length 94;
Best Local Similarity 100.0%; Pred. No. 6.6e-13;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 987 TTGTGTGCTGAAGCTATCTGCCCAAGTTAATGCAAAATGGACACATTTTTTATGTCAGAAA 1046
Db 1 TTGTGTGCTGAAGCTATCTGCCCAAGTTAATGCAAAATGGACACATTTTTTATGTCAGAAA 60
Qy 1047 AAC 1080
Db 61 AAC 94

RESULT 15

US-09-513-999C-24816
; Sequence 24816, Application US/09513999C

; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 24816
; LENGTH: 90
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 23
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 70
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-24816

Query Match 7.0%; Score 77.6; DB 4; Length 90;
Best Local Similarity 96.7%; Pred. No. 4.9e-09;
Matches 88; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 976 CTGTGTTTCTTTGTTGCTGCAAGCTATCTGCCCAAGTTAATGCAATGGACACATTTT 1035
Db 1 CTGTGTTTCTTTGTTGCTGCTGC-ARCTATCTGCCCAAGTTAATGCAATGGACACATTTT 59
QY 1036 TATGTCAGAAAACACACACACACACACACA 1066
Db 60 TATGTCAGAAAACACACACACACACACACACA 90

Search completed: March 30, 2005, 03:12:17
Job time : 233 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 30, 2005, 02:08:00 ; Search time 666 Seconds
(without alignments)
9878.532 Million cell updates/sec

Title: US-10-071-645-1

Perfect score: 1104

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Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 12: /cgn2_6/ptodata/1/pubpna/US09D_PUBCOMB.seq:*
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- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1104	100.0	1104	15	US-10-071-645-1
2	699.8	63.4	1510	10	US-09-820-649-25
3	699.8	63.4	1510	16	US-10-160-162-25
4	699.8	63.4	1510	19	US-10-936-773-25
5	642	58.2	2058	18	US-10-723-860-7058
6	634.6	57.5	1850	14	US-10-198-846-11350
7	632.6	57.3	1321	17	US-10-172-118-1796
8	632.6	57.3	1321	17	US-10-342-887-1796
9	607.2	55.0	3189	15	US-10-071-645-3
10	443.2	40.1	553	17	US-10-136-728-21
11	405.4	36.7	417	11	US-09-978-360A-155
					Sequence 1, Appl1
					Sequence 25, Appl1
					Sequence 25, Appl1
					Sequence 7058, Ap
					Sequence 11350, A
					Sequence 1796, Ap
					Sequence 1796, Ap
					Sequence 3, Appl1
					Sequence 21, Appl1
					Sequence 155, App

12	380.4	34.5	584	13	US-10-027-632-231746	Sequence 231746,
13	380.4	34.5	584	17	US-10-027-632-231746	Sequence 231746,
14	343.8	31.1	366	17	US-10-242-535A-49104	Sequence 49104, A
15	343.8	31.1	366	17	US-10-085-783A-49104	Sequence 49104, A
16	295.8	26.8	360	17	US-10-242-535A-44577	Sequence 44577, A
17	295.8	26.8	360	17	US-10-085-783A-44577	Sequence 44577, A
18	282.2	25.6	411	9	US-09-964-824A-322	Sequence 322, App
19	282.2	25.6	411	9	US-09-954-456-313	Sequence 313, App
20	282.2	25.6	411	9	US-09-954-456-2149	Sequence 2149, Ap
21	282.2	25.6	411	10	US-09-873-367C-677	Sequence 677, App
22	272	24.6	620	14	US-10-198-846-8710	Sequence 8710, Ap
23	270	24.5	417	9	US-09-736-457-475	Sequence 475, App
24	270	24.5	417	9	US-09-902-941-475	Sequence 475, App
25	270	24.5	417	9	US-09-849-636-475	Sequence 475, App
26	270	24.5	417	10	US-09-476-300-475	Sequence 475, App
27	270	24.5	417	14	US-10-017-754-475	Sequence 475, App
28	270	24.5	417	16	US-10-113-872-475	Sequence 475, App
29	270	24.5	417	17	US-10-283-017-475	Sequence 475, App
30	262	23.7	453	14	US-10-060-036-2622	Sequence 2622, Ap
31	259.4	23.5	451	14	US-10-066-543-1967	Sequence 1967, Ap
32	197.8	17.9	549	17	US-10-152-319A-124	Sequence 124, App
33	165	14.9	336	9	US-09-738-973-560	Sequence 560, App
34	165	14.9	336	9	US-09-854-133-560	Sequence 560, App
35	165	14.9	336	15	US-10-144-849A-560	Sequence 560, App
36	162.4	14.7	869	18	US-10-363-345A-29799	Sequence 29799, A
37	162.4	14.7	869	18	US-10-363-345A-29800	Sequence 29800, A
38	160.6	14.5	356	9	US-09-783-590-147	Sequence 147, App
39	149.8	13.6	869	18	US-10-363-345A-29797	Sequence 29797, A
40	149.8	13.6	869	18	US-10-363-345A-29798	Sequence 29798, A
41	141.4	12.8	474	10	US-09-918-995-26636	Sequence 26636, A
42	123.2	11.2	412	14	US-10-198-846-2573	Sequence 2573, Ap
43	118.8	10.8	550	17	US-10-362-674-1	Sequence 1, Appl1
44	118.8	10.8	1222	18	US-10-335-053-193	Sequence 193, App
45	115.8	10.5	433	9	US-09-983-965-2915	Sequence 2915, Ap

ALIGNMENTS

RESULT 1
US-10-071-645-1
; Sequence 1, Application US/10071645
; Publication No. US20030148389A1
; GENERAL INFORMATION:
; APPLICANT: Bihain, Bernard
; APPLICANT: Bougueret, Lydie
; TITLE OF INVENTION: Schizophrenia Related Gene and Protein
; FILE REFERENCE: 92.US2.CIP
; CURRENT APPLICATION NUMBER: US/10/071,645
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/223,482
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: PCR/IS01/01891
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 87..346
US-10-071-645-1

Query Match 100.0%; Score 1104; DB 15; Length 1104;
Best Local Similarity 100.0%; Pred. No. 1.6e-251;
Matches 1104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACGAGCGCGCGCTGACCTGTCCGCGCGCGGGGACGCGCGCGGAGGAGCGG 60

DB 1 GGCACGAGCGCGCGCTGACCTGTCCGCGCGCGGGGACGCGCGCGGAGGAGCGG 60


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QY 1009 CAAGTAATGCAATGGACACATTTTATGTGAGAAAACACACACACACACACACA 1068
Db 901 CAAGTTAATGCAATGGACACATTTTATGTGAGAAAACACACACACACACACACA 960
QY 1069 CACACACACACACACACACACACACACACACACACACACACACACACACACAA 1104
Db 961 CACACACACACACACACACACACACACACACACACACACACACACACACACAAA 996

RESULT 5
US-10-723-860-7058/c
; Sequence 7058, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NFUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7058
; LENGTH: 2058
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1952)..(1952)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2033)..(2033)
; OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-7058

Query Match 58.2%; Score 642; DB 18; Length 2058;
Best Local Similarity 87.3%; Pred. No. 1.le-141;
Matches 838; Conservative 0; Mismatches 90; Indels 32; Gaps 11;

QY 177 GACACCAACAACCTCTTGGCGCGCGGCGGACCAAGCGCGCCGAGCTGGCCAGATC 236
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QY 237 GGCGGAGCAAGCGGCTTATTGAAGATGATAGGATGATGATGCTGCTGAAAAATATG 296
Db 1813 GGCGGAGCAAGCGGCTTATTGAAGATGATAGGATGATGATGCTGCTGAAAAATATG 1754

QY 297 ACCGACAGGCAACCT-CTGGTGTCTAACT-CCCAAGACAATGATGATTAAGGAGAGAT 354
Db 1753 ACCGACAGGCAACCTCTGGTGTCTAACTCCCAAGACAATGATGATTAAGGAGAGAT 1694

QY 355 AGGACAGCGGTAACAGTTATTGGCAAAAGCATGAAAGAGAAAGCACTTTGAAATTTA 414
Db 1693 AGAAGCGGCGTAACAGTTATTGGCAAAAGCATGAAAGAGAAAGCACTTTGAAATTTA 1634

QY 415 TTACTAGCTTG-TACCCAGATGAATCAACAACTGTATCTGGTAT-ATGCCCGGAGAC 472
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QY 473 AGATTAGGCGA-AGGAGGAGAGAGAGAGAAAGGCTTGGGC-CCCTTACAAATATAA 530
Db 1573 AGATGAGGCGAGAGGAGGAGGAGGAGGAGAGAGGCTCTGGCTCCTCTGCAAAATAA 1514

QY 531 TAAATAAATAAATTTAAATAATAAATCCCTATA-----TCCCATAT 574
Db 1513 AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAG 1454

QY 575 AAGAATAAAGAGTCTCACT----GCAGTATTGGCAAAATTAATCAATCTCTTTTAAAT 630
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QY 631 ACGGGAATATT---GGCATTATACATCTGGAATTTTG-ACCACCTTAATGAAGCGC-ACC 684
Db 1393 TACGGTGAATATTGGCGCAATTAAGATCTGGAATTTTGAACCACTTANTGAGCGGCAACA 1334
QY 685 CCAGGTGTTTTGAGGTGTGGCATTCTTTGCGTGATTTGCGTGTCCCAATGTTTACATTA 744
Db 1333 CCAGGTGTTTTGAGGTGTGGCATTCTTTGCGTGAATTTGCGTGTCCCAATGTTTACATTA 1274

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QY 805 TTTTATGTTGTATCTCTTGGATGTACAAAAATTCAGAAAAATGATCTCTGTAGATATTCT 864
Db 1213 TTTTATGTTGTATCTCTTGGATGTACAAAAATTCAGAAAAATGATCTCTGTAGATATTCT 1154

QY 865 GTTTTATTTTGGTCACTCTTTAGAACTTATCAGGAATGTGTTTAAACCAAGAGAGAACTT 924
Db 1153 GTTTTATTTTGGTCACTCTTTAGAACTTATCAGGAATGTGTTTAAACCAAGAGAGAACTT 1094

QY 925 TTCTAAGGAATGATACATAGAAAAGATTTTATTTTAAATGATTTGTTAAAGCTTGTGTTT 984
Db 1093 TTCTAAGGAATGATACATAGAAAAGATTTTATTTTAAATGATTTGTTAAAGCTTGTGTTT 1034

QY 985 CTTTGTGCTGCAAGCTATCTGCCCAAGTTAATGCAAAATGGAACACATTTTATGTGACA 1044
Db 1033 CTTTGTGCTGCAAGCTATCTGCCCAAGTTAATGCAAAATGGAACACATTTTATGTGACA 974

QY 1045 AAAACACACACACACACACACACACACACACACACACACACACACACACACACACAC 1104
Db 973 AAAACACACACACACACACACACACACACACACACACACACACACACACACACACAC 914

RESULT 6
US-10-198-846-11350
; Sequence 11350, Application US/10198846
; Publication No. US20030099974M1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11350
; LENGTH: 1850
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 26, 107, 1839, 1840, 1841, 1842, 1843, 1844, 1845, 1846,
; LOCATION: 1847, 1848, 1849, 1850
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11350

Query Match 57.5%; Score 634.6; DB 14; Length 1850;
Best Local Similarity 86.9%; Pred. No. 5.9e-140;
Matches 833; Conservative 0; Mismatches 94; Indels 32; Gaps 11;

QY 177 GACACCAACAACCTTTCTGGCGCGCGGCGGAGAAACAGCGCGCCCAAGCTGGGCCAGATC 236
Db 192 GAAACCTCGATCGGCTGCGCGCGCTCGCGCGGAGGAGCATGGAGAAGCTGGGCCAGATC 251
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QY 237 GCGCGGAGCAAGCGGTTCTTATGAAGATAGATAGATGATGCTGCTGAAATATG 296
 Db 252 GCGCGGAGCAAGCGGTTCTTATGAAGATAGATAGATGATGCTGCTGAAATATG 311
 QY 297 ACCGACAGGCACTTCTGCTCTAACT-CCCCAAGACAATGATGATTAAGGAGAGAT 354
 Db 312 ACCGACAGGCACTTCTGCTCTAACTCCCCAAGACAATGATGATTAAGGAGAGAT 371
 QY 355 AGGAACGGCGGTAAACAGTTATTTGGCAAAAGATGAAAGAGAAAGCACTTTGAAATTTA 414
 Db 372 AAGAACGGCGGTAAACAGTTATTTGGCAAAAGATGAAAGAGAAAGCACTTTGAAATTTA 431
 QY 415 TTACTAGCTTG-TACCCAGATGAATCAACACCTGTATCTGCTAT-ATGCCGCGAGAC 472
 Db 432 TTACTAGCTTGTTACCCAGATGAATCAACACCTGTATCTGCTATCTGCGCGGAGAC 491
 QY 473 AGATTAGGCGA-AGGAGGAGAGAGAGAGAGAAAGGCTTGGGC-CCTCTACAAATAAAA 530
 Db 492 AGATGAGCGGAGAGGAGGAGGAGGAGAGAGGCTCTGGCTCCTCTGCAAAATAA 551
 QY 531 TAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 574
 Db 552 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 611
 QY 575 AAGAATAAAGAGTCTCACT---GCAGTATTTGGCAAAATAAATAAATAAATAAATAA 630
 Db 612 AATAAATAAAGAGTCTCACTGCGAGCTATTTGTCANAATAAATAAATAAATAAATAA 671
 QY 631 ACGGGAATATT---GGCATTATAGATCTGGAATTTTG-ACCATTAAATGAAGCGC-ACC 684
 Db 672 TACGGTGAATATTGGCAATATTAGATCTGGATTTTGAACCACTTAATGAAGCGCAACA 731
 QY 685 CAGGTGTTTGAAGTGTGGCAATTTCTGCTGATTTGCTGCTGCTGCTGCTGCTGCTGCT 744
 Db 732 CCAGGTGTTTGAAGTGTGGCAATTTCTGCTGATTTGCTGCTGCTGCTGCTGCTGCTGCT 791
 QY 745 TTTAATCTTGAATAAGTCTGCTGCACTTGGATGTAATGCTGCTGCTGCTGCTGCTGCTGCT 804
 Db 792 TTTAATCTTGAATAAGTCTGCTGCACTTGGATGTAATGCTGCTGCTGCTGCTGCTGCTGCT 851
 QY 805 TTTTATGTTGTTATCCTTGGATGTACAAAAATTCAGAAAAATGATCTCTGTAGATTTCT 864
 Db 852 TTTTATGTTGTTATCCTTGGATGTACAAAAATTCAGAAAAATGATCTCTGTAGATTTCT 911
 QY 865 GTTTATTTTGTCTATCTTGAAGTATCAGGAATGTTTAAACAGAGAGACTT 924
 Db 912 GTTTATTTTGTCTATCTTGAAGTATCAGGAATGTTTAAACAGAGAGACTT 971
 QY 925 TTCTAAGGAATGATACATAGAAAAAGTTTATTTTAAATGAGTTGTAAGCTTGTGTTT 984
 Db 972 TTCTAAGGAATGATACATAGAAAAAGTTTATTTTAAATGAGTTGTAAGCTTGTGTTT 1031
 QY 985 CTTTGTGCTGAAGCTATCTGCCAAGTAAATGCAATGGAACACATTTTTTTATGTCAGA 1044
 Db 1032 CTTTGTGCTGAAGCTATCTGCCAAGTAAATGCAATGGAACACATTTTTTTATGTCAGA 1091
 QY 1045 AAAAAAC 1103
 Db 1092 AAAAAAC 1150

RESULT 7

US-10-172-118-1796

; Sequence 1796, Application US/10172118
 ; Publication No. US20030224374A1

GENERAL INFORMATION:

; APPLICANT: Dai, Hongyue
 ; APPLICANT: He, Yudong
 ; APPLICANT: Linsley, Peter
 ; APPLICANT: Mao, Mao
 ; APPLICANT: Roberts, Chris
 ; APPLICANT: Van 't Veer, Laura

; APPLICANT: Van de Vijver, Marc
 ; APPLICANT: Bernards, Rene
 ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
 ; FILE REFERENCE: 9301-175-999
 ; CURRENT APPLICATION NUMBER: US/10/172,118
 ; CURRENT FILING DATE: 2002-06-14
 ; PRIOR APPLICATION NUMBER: 60/380,770
 ; PRIOR FILING DATE: 2002-05-14
 ; NUMBER OF SEQ ID NOS: 2699
 ; SEQ ID NO 1796
 ; LENGTH: 1321
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: NM_018584
 ; DATABASE ENTRY DATE: 2001-06-18
 US-10-172-118-1796

Query Match 57.3%; Score 632.6; DB 17; Length 1321;
 Best Local Similarity 89.0%; Pred. No. 1.5e-139;
 Matches 816; Conservative 0; Mismatches 69; Indels 32; Gaps 11;

QY 220 CCAAGCTGGCGCAGATCGGCGGAGCAAGCGGTTGTTATTGAAGATGATAGGATTTGATG 279
 Db 1 CCAAGCTGGCGCAGATCGGCGGAGCAAGCGGTTGTTATTGAAGATGATAGGATTTGATG 60
 QY 280 ACGTGCTGAAAAATATGACCGCAAGGCACT-CTGGTGTCTAACT-CCCCAAGACAAT 337
 Db 61 ACGTCTGAAAAATATGACCGCAAGGCACTCTCTGGTGTCTAACTCCCCAAGACAAT 120
 QY 338 GAGTTAAGGGAGAGAATAGGAACGGCGGTAAACAGTTATTGGCAAAAGCATGAAAGAGA 397
 Db 121 GAGTTAAGGGAGAGAATAGGAACGGCGGTAAACAGTTATTGGCAAAAGCATGAAAGAGA 180
 QY 398 AAGCACTTTGAAATTTATTACTAGCTTG-TACCCAGATGAATCAACAACTGTATCTG 456
 Db 181 AAGCACTTTGAAATTTATTACTAGCTTGCTACCCAGATGAATCAACAACTGTATCTG 240
 QY 457 GTAT-ATGCCCGGAGACAGATTAGCGA-AGGAGAGAGAGAGAGAGAGAGGCTTGGG 514
 Db 241 GTATCAGCCCGGAGACAGATGAGCGGAGAGAGAGAGAGAGAGAGGCTTGGG 300
 QY 515 C-CCTCTCAAAATAAAATAAAAAAATAAAATTTTAAATTAATAAATCCCTATA----- 566
 Db 301 CTCCTCTCAAAATAAAATAAAAAAATAAAATTTTAAATTAATAAATTTCAATTTCAAC 360
 QY 567 -----TCCCATATAAAGATTAAGACGCTCACT-----GCAGTATGGCAAAATTA 613
 Db 361 TATATACACATATAAAGAAATAAAAGAAAGTCTCAGTTGCGAGCTATTTGTCAAAATTAAT 420
 QY 614 ATCCATTTCTTTTAAATACGGG---AATATTGGCATTATAGATCTGATTTTG-ACCAC 668
 Db 421 ATCCATTTCTTTTATATACGGTGAATATGCGCAATTAAGATCTGATTTTGAACAC 480
 QY 669 TTAATGAAGCGGC-ACCCAGGTGTTTGAAGTGTGGCATTCTTCGCTGATTTGCGTGT 727
 Db 481 TTAATGAAGCGGCACACACAGGTGTTTGAAGTGTGGCATTCTTCGCTGATTTGCGTGT 540
 QY 728 TCCCAATGTTTACATTTTAACTCTGCAAAATGGTCTGTGCACTTTGGATGTGAATG 787
 Db 541 TCCCAATGTTTACATTTTAACTCTGCAAAATGGTCTGTGCACTTTGGATGTGAATG 600
 QY 788 CTGTCAGTTTATTTTATTTTATGTTTATCTCTGGATGTACAAAAATTCAGAAAAATG 847
 Db 601 CTGTCAGTTTATTTTATTTTATGTTTATCTCTGGATGTACAAAAATTCAGAAAAATG 660
 QY 848 ATCTCTGTAGATATTCTGTTTATTTTTCGTCACTCTTTAGAGTATACAGGAATGTGTTA 907
 Db 661 ATCTCTGTAGATATTCTGTTTATTTTTCGTCACTCTTTAGAGTATACAGGAATGTGTTA 720
 QY 908 AAACAGAGAGAGAACTTTTCTAAGGAATGATACATAGAAAGATTTTATTTAAATGAG 967
 Db 721 AAACAGAGAGAGAACTTTTCTAAGGAATGATACATAGAAAGATTTTATTTAAATGAG 780

Qy	968	TTGTAAGCGTTGTGTTCTTTGTTGCTGCAAGCTATCTGCCCAGTAAATGCAAAATGGAC	1027
Db	781	TTGTAAGCGTGTGTTCTTTCTTTGTTGCTGCAAGCTATCTGCCCAGTAAATGCAAAATGGAC	840
Qy	1028	ACATTTTTTTATGTCAGAAAAAC	1087
Db	841	ACATTTTTTTATGTCAGAAAAAC	900
Qy	1088	AAAAAAAAAAAAAAAAAAAA 1104	
Db	901	ACGAAAAACCAAGAAAA 917	
RESULT 8			
US-10-342-887-1796			
; Sequence 1796, Application US/10342887			
; Publication No. US20040058340A1			
; GENERAL INFORMATION:			
; APPLICANT: Dai, Hongyue			
; APPLICANT: He, Yudong			
; APPLICANT: Linsley, Peter S.			
; APPLICANT: Mao, Mao			
; APPLICANT: Roberts, Christopher J.			
; APPLICANT: Van 't Veer, Laura Johanna			
; APPLICANT: Van de Vijver, Marc J.			
; APPLICANT: Bernards, Rene			
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients			
; FILE REFERENCE: 9301-188-999			
; CURRENT APPLICATION NUMBER: US/10/342,887			
; CURRENT FILING DATE: 2003-01-15			
; PRIOR APPLICATION NUMBER: 60/298,918			
; PRIOR FILING DATE: 2001-06-18			
; PRIOR APPLICATION NUMBER: 60/380,710			
; PRIOR FILING DATE: 2002-05-14			
; PRIOR APPLICATION NUMBER: 10/172,118			
; PRIOR FILING DATE: 2002-06-14			
; NUMBER OF SEQ ID NOS: 2699			
; SEQ ID NO 1796			
; LENGTH: 1321			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-342-887-1796			

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RESULT 9
US-10-071-645--3
; Sequence 3, Application US/10071645
; Publication No. US20030148389A1
; GENERAL INFORMATION:
; APPLICANT: Bihaire, Bernard
; APPLICANT: Bour, Barbara
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Schizophrenia Related Gene and Protein
; FILE REFERENCE: 92.US2.CIP
; CURRENT APPLICATION NUMBER: US/10/071,645
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/223,482
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: PCT/IB01/01891
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent.pm
; SEQ ID NO 3
; LENGTH: 3189
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-071-645--3

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	Query Match	55.0%	Score 607.2;	DB 15;	Length 3189;
	Best Local Similarity	89.2%;	Pred. No. 2.5e-133;		
	Matches 787;	Conservative	0;	Mismatches 63;	Indels 32; Gaps 11;
Qy	252	GTGTGTTATTGAAGATGATAGGATTGATGACGTCCTGAAAAAATATGACCGCAACAGGCACCT	311		
Db	2158	GTGTGTTATTGAAGATGATAGGATTGATGACGTCCTGAAAAAATATGACCGCAACAGGCACCT	2217		
Qy	312	-CTGGTGTCCTAACT-CCCCAAAGACAAATGAGTTAAGGGGACAGATAAGGAAACGCGCGTAAAC	369		

Db 361 ATTGCAAAAGCATGAAAGAGAAAGCACTTTGAAATTTATTACTAGCTTCTACCCAC 420
QY 433 GATGAATCAACAACCTGTATCTGGTAT-ATCCCGGAGACAGATTTAGCGGA-AGGAGGA 490
Db 421 GATGAATCAACAACCTGTATCTGGTATCAGCGCGGAGACAGATCAGCGGAGAGGA 480
QY 491 AGAGAGAGAGAAAGGCTTGGGCCCTCTACAATAAATAAATAAATAAATAAATAAATAA 550
Db 481 GGAGGAGGAGGAGAGGCTCTGGGGCTCTCTGCAAAAAAATAAATAAATAAATAAATAA 540
QY 551 TAATAAAA 558
Db 541 AAAAAAAA 548

RESULT 11
US-09-978-360A-155
; Sequence 155, Application US/09978360A
; Publication No. US20040110939A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.US4.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; PRIORITY FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 155
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 327..416
; FEATURE:
; NAME/KEY: polyA site
; LOCATION: 404..417
US-09-978-360A-155

Query Match 36.7%; Score 405.4; DB 11; Length 417;
Best Local Similarity 98.6%; Pred. No. 6.6e-86;
Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 690 TGTGTTGAGGTGTGGCATTTCTGGCTGATTTGGCTGTTCCCAATGTTTACATTTAA 749
Db 1 TGTGTTGAGGTGTGGCATTTCTGGCTGATTTGGCTGTTCCCAATGTTTACATTTAA 60
QY 750 TCTTGCAAAATGGTTCTGTGCACTTGGATGTGAAATGCTGCCAGTTTATTTTTTTTA 809

Db 61 TCTTGCAAAATGGTTCTGTGCACTTGGATGTGAAATGCTGCCAGTTTATTTTTTTA 120
QY 810 TGTGTTATCCTTGGATGTACAAAAATTCAGAAAAATGATCTCTGTAGATATTTCTGTTT 869
Db 121 TGTGTTATCCTTGGATGTACAAAAATTCAGAAAAATGATCTCTGTAGATATTTCTGTTT 180
QY 870 ATTTTGGTCATCTTTTGAAGTTATCAGGAATGTGTTTTAAAAACAAGAGAACTTTTCTA 929
Db 181 ATTTTGGTCATCTTTTGAAGTTATCAGGAATGTGTTTTAAAAACAAGAGAACTTTTCTA 240
QY 930 AGGAATGATACATAGAAAAAGATTTTATTTTAAATGAGTTGTAAAGCTTGTCTTTCTTG 989
Db 241 AGGAATGATACATAGAAAAAGATTTTATTTTAAATGAGTTGTAAAGCTTGTCTTTCTTG 300
QY 990 TTGCTGCAAGCTATCTGCCCAAGTTAATGCAAAATGGACACATTTTATGTGCAAAAAAC 1049
Db 301 TTGCTGCAAGCTATCTGCCCAAGTTAATGCAAAATGGACACATTTTATGTGCAAAAAAC 360
QY 1050 AC 1104
Db 361 ACACACACACACACACACATATACACACACACACACACACACACACACACACACAC 415

RESULT 12
US-10-027-632-231746
; Sequence 231746, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIORITY FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231746
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(584)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-231746

Query Match 34.5%; Score 380.4; DB 13; Length 584;
Best Local Similarity 98.0%; Pred. No. 6.8e-80;
Matches 384; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 713 CGCTGATTTGGCTGTTCCTCCCAATGTTTACATTTAAATCTTCCAAAAATGGTTCTGTGCA 772
Db 1 CGCTGATTTGGCTGTTCCTCCCAATGTTTACATTTAAATCTTCCAAAAATGGTTCTGTGCA 60
QY 773 CTTGGATGTGAAATGCTGTCCAGTTTATTTTTTATGTTGTTATCTTGGATGTACAA 832
Db 61 CTTGGATGTGAAATGCTGTCCAGTTTATTTTTTATGTTGTTATCTTGGATGTACAA 120

QY 1091 AAAAAA 1097
|||||
Db 360 AAAACA 366

RESULT 15

US-10-085-783A-49104
; Sequence 49104, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49104
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-49104

Query Match 31.1%; Score 343.8; DB 17; Length 366;
Best Local Similarity 97.8%; Pred. No. 2.6e-71;
Matches 359; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 731 CAATCTTACATATTAATCTTGCAAAATGGTCTGTCGACCTGGATGTCAAAATGCTG 790
Db 1 CAATGTTACATATTAATCTTGCAAAATGGCTCTGTCGACCTGGATGTCAAAATGCTG 60

QY 791 TCCAGTTTATTTTATTTTATGTTTATCTCTGGATGTACAAAAATTCAGAAAAATGATC 850
Db 61 TCCAGTTTATTTTATTTTATGTTTATCTCTGGATGTACAAAAATTCAGAAAAATGATC 120

QY 851 TCTGTAGATATTCGTGTTTATTTTGGTCAATCTTTAGAGTTATCAGGAATGTGTTAAAA 910
Db 121 TCTGTAGATATTCGTGTTTATTTTGG-CATCTTTAGAGTTATCAGGAATGTGTTAAAA 179

QY 911 CAAGAAGAGAACTTTTCTAAGGAATGATACATAGAAAGATTTTATTTAAATCAGTTG 970
Db 180 CAAGAAGAGAACTTTTCTAAGGAATGATACATAGAAAGATTTTATTTAAATCAGTTG 239

QY 971 TAAAGCTTGTGTTTCTTTGCTGCAAGCTATCTGCCCAAGTTAATGCAAAATGGACACA 1030
Db 240 TAAAGCTTGTGTTTCTTTGCTGCAAGCTATCTGCCCAAGTTAATGCAAAATGGACACA 299

QY 1031 TTTTATGTCAGAAAAAC 1090
Db 300 TTTTATGTCAGAAAAAC 359

QY 1091 AAAAAA 1097
|||||
Db 360 AAAACA 366

Search completed: March 30, 2005, 05:50:57
Job time : 670 secs

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OM nucleic - nucleic search, using sw model

Run on: March 29, 2005, 18:29:28 ; Search time 3513 Seconds
(without alignments)
11962.127 Million cell updates/sec

Title: US-10-071-645-1
Perfect score: 1104
Sequence: 1 ggcacgagcgagcgccgctg.....aaaaaaaaaaaaaaaaaaaa 1104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_ges1:
9: gb_ges2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	623	56.4	954	7 CN643673	CN643673 ILLUMIGEN
3	615.6	55.8	945	7 CN803102	CN803102 ILLUMIGEN
4	614.4	55.7	976	7 CN802133	CN802133 ILLUMIGEN
5	611.8	55.4	953	7 CN803224	CN803224 ILLUMIGEN
6	611.2	55.4	950	7 CN646790	CN646790 ILLUMIGEN
7	610.8	55.3	954	7 CN646555	CN646555 ILLUMIGEN
8	610.2	55.3	954	7 CN646445	CN646445 ILLUMIGEN
9	609.6	55.2	952	7 CN646545	CN646545 ILLUMIGEN
10	608.2	55.1	951	7 CN647038	CN647038 ILLUMIGEN
11	607.2	55.0	1566	3 CR604926	CR604926 full-leng
12	606.4	54.9	955	7 CN644007	CN644007 ILLUMIGEN
13	605.4	54.8	954	7 CN803392	CN803392 ILLUMIGEN
14	599.6	54.3	953	7 CN846019	CN846019 ILLUMIGEN
15	589.8	53.4	964	7 CN646785	CN646785 ILLUMIGEN
16	586.6	53.1	955	7 CN805169	CN805169 ILLUMIGEN
17	581.6	52.7	955	7 CN802272	CN802272 ILLUMIGEN
18	580.2	52.6	951	7 CN802081	CN802081 ILLUMIGEN
19	579.8	52.5	1020	7 CN803473	CN803473 ILLUMIGEN
20	574.8	52.1	944	7 CN803534	CN803534 ILLUMIGEN
21	574.4	52.0	955	7 CN801954	CN801954 ILLUMIGEN
22	557.2	50.5	1026	7 CN643857	CN643857 ILLUMIGEN
23	550.6	49.9	993	7 CN802904	CN802904 ILLUMIGEN
24	548.8	49.7	956	7 CN805265	CN805265 ILLUMIGEN

25	542.8	49.2	911	7	CN802110	CN802110 ILLUMIGEN
26	532.6	48.2	967	7	CN644185	CN644185 ILLUMIGEN
27	520.8	47.2	967	7	CN641685	CN641685 ILLUMIGEN
28	515.2	46.7	968	7	CN805606	CN805606 ILLUMIGEN
29	511.2	46.3	806	7	CN642220	CN642220 ILLUMIGEN
30	503.4	45.6	1001	7	CN802311	CN802311 ILLUMIGEN
31	500.4	45.3	1004	7	CN801895	CN801895 ILLUMIGEN
32	499.6	45.3	983	7	CN803331	CN803331 ILLUMIGEN
33	496	44.9	890	7	CO645235	CO645235 ILLUMIGEN
C 34	489.6	44.3	747	5	BQ018543	BQ018543 UI-H-DH1-
35	483	43.8	981	7	CN801823	CN801823 ILLUMIGEN
36	471.2	42.7	914	7	CO645211	CO645211 ILLUMIGEN
37	463.2	42.0	819	4	BI553632	BI553632 603190553
C 38	447.8	40.6	953	7	CO645289	CO645289 ILLUMIGEN
C 39	446	40.4	597	7	W17400	W17400 zbl5b10.r1
C 40	445.2	40.3	661	5	BQ000750	BQ000750 UI-H-DH1-
41	444.2	40.2	1083	3	CR606015	CR606015 full-leng
C 42	441	39.9	676	5	BQ771726	BQ771726 UI-H-E21-
43	440.6	39.9	931	5	EX419572	EX419572 BX419572
44	437.4	39.6	695	7	CN428017	CN428017 170060000
45	435.8	39.5	808	5	BU570962	BU570962 AGENCOURT

ALIGNMENTS

RESULT 1
AF116637/c 1321 bp mRNA linear HTC 08-MAY-2001

LOCUS AF116637 Homo sapiens PRO1489 mRNA, complete cds.
DEFINITION AF116637
ACCESSION AF116637 GI:7959775
VERSION AF116637.1
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1321)
AUTHORS Zhang, C., Yu, Y., Zhang, S., Wei, H., Zhou, G., Ouyang, S., Luo, L., Bi, J., Liu, M. and He, F.
TITLE Functional prediction of the coding sequences of 121 new genes deduced by analysis of cDNA clones from human fetal liver
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1321)
AUTHORS Zhang, C., Yu, Y., Zhang, S., Wei, H., Zhou, G., Ouyang, S., Luo, L., Bi, J., Liu, M. and He, F.
TITLE Direct Submission
JOURNAL Submitted (24-DEC-1998) Department of Experimental Hematology, Institute of Radiation Medicine, Beijing Taiping Road 27, Beijing 100850, P. R. China
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="FLB5706"
/tissue_type="liver"
/dev_stage="fetal"
complement(991..1152)
/note="predicted protein of HQ1489"
/codon_start=1
/product="PRO1489"
/protein_id="AAF71060.1"
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/translation="MKRESTLKFTSLPTMKSTTCIWIYQAGRQMRREBEEBEEKALGSSAKIKKK"
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Best Local Similarity 89.0%; Pred. No. 5.5e-124;
Matches 816; Conservative 0; Mismatches 69; Indels 32; Gaps 11;
ORIGIN
220 CCAAGCTGGCCAGATCGCCGAGCAAGCGGTTGTTATTGAAGATGATAGGATTGATG 279

		Query Match	55.4%; Score 611.2; DB 7; Length 950;	
		Best Local Similarity	87.3%; Pred. No. 1.9e-119;	
		Matches	829; Conservative	0; Mismatches 83; Indels 38; Gaps 13;
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Qy	185	CAACCTCTTCGGCGCCGCGCAGACACAGCGCGCCGCCAAGCTGGCCAGATCGGCCGAG	244	
Dd	1			
Qy	245	CAAGCGGGTGTATTGAAGATGATAGGATTGATGACTGTGCTGAAAAATATGACGCACA	304	
Dd	61			
Qy	305	GACACT-CTGGTGCTAACT-CCCCAAAAGACAATGAGTTTAAGGGAGAGAATAGAACGG	362	
Dd	121	GGCACCTCTCTGGTGTCTAACTCCCCCAAAGACAATGAGTTTAAGGGAGAGAATAAGAACGG	180	
Qy	363	CGGTAAACAGTTATTGGCAAAAGCATGA AAAAGAGAAAGCACTTTGAAATTTATTACTAGC	422	
Dd	181	CGATACAGTTACTGGCAAAAGCATGAAAACAGAAAGCACTTTGAAATTTATTACTAGC	240	
Qy	423	TTC-TACCCACGATGAAATCAACACCTGTATCTGGTAT-ATGCCCGGAGACAGATTAGG	480	
Dd	241	TTGCTACCCACGATGAAATCAACACCTGTATCTGGTATCAGGCCGGAGACAGATGAGG	300	
Qy	481	C-----GAAGGAGGAAGAGAGAGAGAAAGGCTTGGCCCTCTACAAATAAATAA	533	
Dd	301	CGTGAGAAAGGAGGAGGAGGAGGCTCTGGGCTTCTCTGCAAAAATAAAAATAA	360	
Qy	534	AAAAAAAAATTTAAA---ATAATPAAAAATCCCTATATCC-----CATATAAGAAATAAA	583	
Dd	361	TAAATAAAATTTAAAAATAAATAAATAACATATATACACATATAAGAAATAA	420	
Qy	584	AGAGTCTCAGT----GCAGTATTGGCAAAAATTAATCCAATTCCTTTTTTAATACGGGAATA	639	
Dd	421	GAAGTCTCAGTTGCAGCTATTTTGTCAAAAATTAATCCAATTCCTTTTTATATACGGTGA	480	
Qy	640	TT----GGCAATTATAGATCTGGATTTTG-AACCCTTAATGAAGCGGC-ACCCAGAGTGT	693	
Dd	481	TATTGCCAATTATAGATCTGGATTTTGAAACCCTTAATGAAGCGGCACACACCGAGTATT	540	
Qy	694	TTGAGTGTGGCANCTCTCGCTGATTTGGCTGTTCCTCAATGTGTTACATTTTAATCTTT	753	
Dd	541	TTGAGTGTGGCAATCTTCGCTGATTTGGCTGTTCCTCAATGTGTTACATTTTAATCTTT	600	
Qy	754	GCAAAATGGTTCGTGTCACCTTGGATGTGAAATGCTGTCAGTTTTATTTTTTATGTT	813	
Dd	601	GCAAAATGGTTCGTGTCACCTTGGATGTGAAATGCTGTCAGTTTTATTTTTTATGTT	660	
Qy	814	GTTATCCTTGGATGTACAAAAATTCAGAAAAATGATCTGTGATAGATATCTGTTTTATTT	873	
Dd	661	GTTATCCTTGGATGTACAAAAATTCAGAAATATGATCTGTGATAGATATCTGTTTTATTT	720	
Qy	874	TGTCATCTTTTAGAAGTTATCAGGAATGTGTTTAAAAACAAGAGAGAACTTTTCTAAGGA	933	
Dd	721	TGTCATCTTTTAGAAGTTATCAGGAATGTGTTTAAAAACAAGAGAGAACTTTTCTAAGGA	780	
Qy	934	ATGATACATAGAAAAG- ----TTTTTATTTTAAAAATGAGTTGTAAAGCTTGTTCTTT	987	
Dd	781	ATGATACATAGAGAGATCTCTGTTTATTTTAAAAATGAGTTGTAAAGCTTGTTCTTT	840	
Qy	988	TGTTGCTGCAAGCTATCTGCCCAAGTTAAATGCAAAATGGACACATTTTTTTTATGTGAGAAA	1047	
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Qy	1048	AC	1097	
Dd	901	ACACACACACACACAC-CCCACCCACGACACCCACCAACCAACCAACCAACCAACCAAC	949	

RESULT 7	linear	EST	13-MAY-2004
CN646555	954 bp	linear	EST
CN646555	954 bp	linear	EST
LOCUS	954 bp	linear	EST

DEFINITION	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT
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ILLUMIGEN MQC 26331 Katze MMRB Macaca mulatta cDNA clone IBIUW:8439
5' similar to Bases 1 to 360 highly similar to human CAMK1NA1alpha
(Hs.197922), mRNA sequence.
CN646555
CN646555.1 GI:47159998
EST.
Macaca mulatta (rhesus monkey)
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
1 (bases 1 to 954)
Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.03.10. 788 Q20 bases.
PCR Primers
FORWARD: CCTCACTAAAGGGACAAA
BACKWARD: CACTATAGGGCGAATTGGTA
Insert Length: 954 Std Error: 0.00
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Seq primer: CCTCACTAAAGGACAAA
polyA=yes.

FEATURES
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/clone="IBIUM:8439"
/sex="female"
/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katzke MWBF"
/note="Organ: brain; Vector
Site: 2; Xho I; Created from
kit (catalog #200400) and
Cloning kit (Catalog #2004
#2004)"
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ORIGIN

Query Match	55.3%	Score 610.8	DB 7	Length 954
Best Local Similarity	87.0%	Pred. No. 2.3e-119		
Matches 830	Conservative 0	Mismatches 87	Indels 37	Gaps 13
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Db	1	CAACTCTTCGCGCGCGGAGACAACGCGCGCGCCCAAGCTGGCCAGATCGGCCGGAG	60	
QY	245	CAAGCGGGTGTATTGAAGATGATAGGATTGATGACGTCTGAAAAAATATGACGCACA	304	
Db	61	CAAGCGGGTGTATTGAAGATGATAGGATTGATGACGTCTGAAAAAATATGACGCACA	120	
QY	305	GGCACCCTCTGGTGTCTAACTCCCCAAAGACAATGAGTTAAGGGAGAGAAATAGGAACGG	362	
Db	121	GGCACCCTCTGGTGTCTAACTCCCCAAAGACAATGAGTTAAGGGAGAGAAATAGGAACGG	180	
QY	363	CGGTAAACAGTTATTGGCAAAAACGATGAAAAGAGAAAGCACTTTGAAATTTTATTACTAGC	422	
Db	181	CGATAACAGTTACTTGGCAAAAACGATGAAAACAGAAAGCACTTTGAAATTTTATTACTAGC	240	
QY	423	TTGCTACCCACGATGAAATCAACAACTGTATCTGGTATATGCGCGGAGACAGATTAGG	480	
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QY	481	C-----GAAGGAGGAAGAGAGAGAAAGGGCTTGGCGCCCTCTACAAATAAAAAATAA	533	
Db	301	CGTGAGAAAGAGACAGAGAGAGAAAGGCTCTGGGCTTCTCTCAAAAAATAAAAAATAAATAA	360	


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QY 534 AAAAAAAAAATTTAAA-----ATAATAAATCCCTATATCC-----CATATAAGAAATAAA 583
Db 361 TAAATAAATAATTTAAATAATAATAAATAATCACTATATACACATATAAAGAAATAAATAA 420
QY 584 AGAGTCTCAGT-----GCAGTATGCGAATAATTAATCCATTTCTTTTAAATACGG----- 635
Db 421 GAAGTCTCAGTGTGCGAGTATTTGTCAAAATTAATATATCCATTTCTTTTATATACGGTGA 480
QY 636 AATATGCGCATATATAGATCTGATTTTGA-CCACTTAATGAAGCGC-ACCCACAGTGT 693
Db 481 TATTCGCGCATATATAGATCTGATTTTGNACCACTTAATGAAGCGCGCAACACAGTATT 540
QY 694 TTGAGGTGTGCGCATTTCTGCTGATTTGCTGTTTCCCAATGTTTACATTTATTTAATCTT 753
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QY 754 GCAAAATGGTCTCTGCACTTGGATGGAATGCAATGCTGCTCCAGTTTATTTTATGTT 813
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QY 814 GTTATCTTGGATGTACAAAAAATTCAGAAATGATCTCTGATATATTTCTGTTTATTT 873
Db 661 GTTATCTTGGATGTACAAAAAATTCAGAAATGATCTCTGATATATTTCTGTTTATTT 720
QY 874 TGGTCATCTTTAGAAAGTTATCAGGAATGTGTTTAAAAACAAGAGAGAACTTTTCTAAGGA 933
Db 721 TGGTCATCTTTAGAAAGTTATCAGGAATGTGTTTAAAAACAAGAGAGAACTTTTCTAAGGA 780
QY 934 ATGATACATAGAAAGAT-----TTTATTTTAAATGAGTTGTAAGCTGTGTTTCTTT 988
Db 781 ATGATACATAGAAAGATCTTGTGTTTATTTTAAATGAGTTGTAAGCTGTGTTTCTTT 840
QY 989 GTTGCTGCAAGCTATCTGCCAAGTTAATGCAATGGACACATTTTATGTCAGAAAAA 1048
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Db 901 CACACACACAC-CCCAACCCCAACACACACACACACACACACACACACACACACACACAC 953

RESULT 8
CN646445
LOCUS
DEFINITION
ILLUMIGEN MCQ 26221 Katze.MBR Macaca mulatta cDNA clone IBUM.8553
5' similar to Bases 1 to 360 highly similar to human CamKIIalpha
(Hb.197922), mRNA sequence.
ACCESSION
CN646445
VERSION
EST.
KEYWORDS
CN646445.1 GI:47159888
SOURCE
Macaca mulatta (rhesus monkey)
ORGANISM
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Macaca.
1 (bases 1 to 954)
Katze.M.G., Thomas.M., Korth.M., Iadonato,S.P. and Magness,C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.03.09. 788 Q20 bases.
PCR Primers
FORWARD: CCCTCACTAAAGGGAACAAA
BACKWARD: CACTATAGCGGATTCGGTA
Insert Length: 954 Std Error: 0.00
Plate: CL000118 row: D column: 02
Seq primer: CCCTCACTAAAGGGAACAAA

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POLYA=Yes.

FEATURES

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Location/Qualifiers
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/db_xref="taxon:9544"
/clone="IBUM:8553"
/sex="female"
/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze.MBR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Stratagene ZAP-cDNA synthesis
kit (catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"

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ORIGIN

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Best Local Similarity 86.4%; Pred. No. 3.1e-119;
Matches 823; Conservative 0; Mismatches 93; Indels 37; Gaps 12;

QY 185 CAACCTTCTTCGCGCGCGGAGAACAGCGCGCGCCCAAGCTGGGCCAGATCGGCGGAG 244
Db 1 CAACCTTCTTCGCGCGCGGCGAGAACAGCGCGCGCCCAAGCTGGGCCAGATCGGCGGAG 60
QY 245 CAAGCGGCTGCTTATTGAAGATGATAGGATTTGATGACCTGCTGAAAAATATGACCGACAA 304
Db 61 CAAGCGGCTGCTTATTGAAGATGATAGGATTTGATGACCTGCTGAAAAATATGACCGACAA 120
QY 305 GGCACCT-CTGGTGTCTAACT-CCCCAAAGACAATAGTTAAGGAGAGAAATAGGAACGG 362
Db 121 GGCACCTCTCTGTCTAACTCCCCCAAGACAATAGTTAAGGAGAGAAATAGGAACGG 180
QY 363 CGGTAACAGTTATTGGCAAAAGCATGAAAGAGAAAGCACTTTTGAAATTTTACTACTAGC 422
Db 181 CGAATAACAGTTACTGGCAAAAGCATGAAAGAGAAAGCACTTTTGAAATTTTACTACTAGC 240
QY 423 TTG-TACCCACGATGAATCAACACCTGTATCTGGTAT-ATGCCCGGAGACAGATTAGG 480
Db 241 TTGCTACCCACGATGAATCAACACCTGTATCTGGTATCAGCCCGGAGACAGATTAGG 300
QY 481 C-----GAAGGAGGAAGAGAGAGAGAAAGCTTTGGGCGCTCTTCAATAAATAAATAA 533
Db 301 CGTGAGAGAGGAGGAGGAGAGAGAGCTCTGGGCTTCTCTGCAAAATAAATAAATAAATAA 360
QY 534 AAAAAAAAAATTTAAA---ATAATAAATCCCTATATCC-----CATATAAGATATAA 583
Db 361 TAAATAAATAATTTAAAAATAATAAATAATCACTATATACACATATAAAGAAATAAATAA 420
QY 584 AGAGTCTCAGT-----GCAGTATTGCAAAATTAATAATCCATTTCTTTTAAATACGG----- 635
Db 421 GAAGTCTCAGTGTGCGCATTTTGTTCAAAATTAATATCCATTTCTTTTATATACGGTGA 480
QY 636 AATATGCGCATATATAGATCTGATTTTGA-CCACTTAATGAAGCGGC-ACCCACAGTGT 693
Db 481 TATTCGCGCAATATATAGATCTGATTTTGAACCACTTAATGAAGCGCGCAACACAGTATT 540
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QY 754 GCAAAATGGTCTCTGCACTTGGATGGAATGCTGCTCCAGTTTATTTTATGTT 813
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QY 874 TGGTCATCTTTAGAAAGTTATCAGGAATGTTTAAAAACAAGAGAGAACTTTTCTAAGGA 933
Db 721 TGGTCATCTTTAGAAAGTTATCAGGAATGTTTAAAAACAAGAGAGAACTTTTCTAAGGA 780

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Db		421	GAAGTCTCAGTTGCAGCTATTGTCAAAAATTAATATCCATTTCTTTTTATATACGGTGAA	480
Qy		636	AATAATTGGCAATTAPAGATCTGGATTTTTGA-CCACTTAATGAAGCGG-C-ACCCEAGGTGTT	693
Db		481	TATTGCCAATATATAGATCTGGATTTTGAACCACTTAATGAAGCGGCAACACACAGGTATT	540
Qy		694	TTGAGGTGTGGCAATCTTCGCTGATTTGGCTGTTCCCAATGTTTACATATTAAATCTT	753
Db		541	TTGAGGTGTGGCAATCTTCGCTGANTGGCTGTTCCCAATGTTTACATATTAAATCTT	600
Qy		754	GCAAAAATGGTTCCTGTGCATCTGGATGTGAATGCTGTCCAGTTTTATTTTTTATGTT	813
Db		601	GCAAAAATGGTTCCTGTGCATCTGGATGTGAATGCTGTCCAGTTTTATTTTTTATGTT	660
Qy		814	GTTATCCTTGGATGTACA AAAAATT CAGAAAATGATCTCTGTAGATATTCTGTTTATTT	873
Db		661	GTTATCCTTGGATGTACA AAAAATT CAGAAAATGATCTCTGTAGATATTCTGTTTATTT	720
Qy		874	TGGTCATCTTTAGAAGTTATCAGGAATGTGTTTAAAAACAAGACAGAACCTTTCTCAAGGA	933
Db		721	TGGTCATCTTTAGAAGTTATCAGGAATGTGTTTAAAAACAAGACAGAACCTTTCTCAAGGA	780
Qy		934	ATGATACATAGAAAAGA-----TTTTTATTTTAAAAATGAGTTGTAAAGCTTGTTTCTT	987
Db		781	ATGATACATAGAAAAGAATCCTTGTTTATTTTAAAAATGAGTTGTAAAGCTTGTTTCTT	840
Qy		988	TGTTGCTGCAAGCTATCTGCCCAAGTTAATGCAAAATGGACACATTTTTTTATGTCAGAAA	1047
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Qy		1048	ACACACACACACACACACACACACACACACACACACGAAAAAAAAAAAAAAAAA	1101
Db		901	ACACCAACCCGCCCCACGCCGCCGCCGCCGCCCAACCAAAAAACAAAAA AAAAAA	954

RESULT 13	CN803392	954 bp	linear	EST 26-MAY-2004
LOCUS	ILLUMIGEN MCQ 32916	Katze MMR	Macaca mulatta	cDNA clone
DEFINITION	IGUW:14140	57 similar to	Bases 61 to 924	highly similar to human
	CAMKIIA1pha	(Hs.197922),	mRNA	sequence.
ACCESSION	CN803392			
VERSION	CN803392.1	GI:47699368		
KEYWORDS	EST.			
SOURCE	Macaca mulatta	(rhesus monkey)		
ORGANISM	Macaca mulatta			
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;			
	Cercopithecinae; Macaca.			
	1 (bases 1 to 954)			
REFERENCE	Katze, M.C., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.			
AUTHORS	Large-scale Rhesus Macaque cDNA sequencing			
TITLE				

FEATURES	Location/Qualifiers source
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:	: 1..954
781 ATGATACATAGAAAAAGATCCTTGTTTTTAATATGAGTTGTAAAGCTTGTTTTCTT 840	Dd
988 TTTTGGTCGAAGCTATCTGCCCAAGTTAATGCAAATGGACAACACTTTTTTTATGTCAGAAA 1047	Qy

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